

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 19:21:50 ; Search time 6639 Seconds  
(without alignments)  
11327.334 Million cell updates/sec

Title: US-10-626-445-5  
Perfect score: 1176  
Sequence: 1 agtgcgagctcaacagctac.....accagtcagtcattcttttga 1176

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1176	100.0	1538	6	AF358859 Mus muscu
2	958.4	81.5	1593	6	AF358860 Rattus no
3	838	71.3	1308	6	BC111862 Mus muscu
4	821.4	69.8	199837	6	AC131672 Mus muscu
5	686.6	58.4	1173	2	AR142850 Sequence
6	686.6	58.4	1173	2	BD015847 Novel pol
7	686.6	58.4	1173	2	CS173186 Sequence
8	686.6	58.4	1173	2	CS178018 Sequence
9	686.6	58.4	1173	2	AR391860 Sequence
10	686.6	58.4	1173	2	AX109119 Sequence
11	686.6	58.4	1173	2	AX139113 Sequence
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13	686.6	58.4	1173	5	AF329449 Homo sapi
14	686.6	58.4	1173	5	AY008280 Homo sapi
15	686.6	58.4	1173	5	AY136745 Homo sapi
16	686.6	58.4	1173	5	AJ298292 Homo sapi
17	686.6	58.4	1266	1	AX376577 Sequence
18	686.6	58.4	1300	2	AX301229 Sequence

19	686.6	58.4	1312	2	BD095598	BD095598 Novel gua
20	686.6	58.4	1312	5	AB045370	AB045370 Homo sapi
21	686.6	58.4	1316	5	BC069136	BC069136 Homo sapi
22	686.6	58.4	1847	5	BC112348	BC112348 Homo sapi
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25	685	58.2	1227	2	BD097512	BD097512 Novel gua
26	685	58.2	1265	5	AB044934	AB044934 Homo sapi
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28	683.4	58.1	1173	5	AF307973	AF307973 Homo sapi
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30	651	55.4	236694	12	AC118386	AC118386 Rattus no
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34	442	37.6	166206	12	AC009668	AC009668 Homo sapi
35	442	37.6	167296	12	AP002507	AP002507 Homo sapi
36	442	37.6	169144	5	AC090244	AC090244 Homo sapi
37	442	37.6	184938	12	AP002476	AP002476 Homo sapi
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39	371	31.5	1950	2	CQ947118	CQ947118 Sequence
40	284.4	24.2	528	5	AY561469	AY561469 Pan trogl
41	283.8	24.1	522	5	AY561470	AY561470 Gorilla g
42	271.6	23.1	1326	2	AX451922	AX451922 Sequence
43	270.6	23.0	429	2	CQ727333	CQ727333 Sequence
44	178	15.1	1249	6	AF267538	AF267538 Cavia por
45	172.8	14.7	1239	2	E39806	E39806 Novel guano

ALIGNMENTS

RESULT 1  
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LOCUS Mus musculus histamine H4 receptor mRNA linear ROD 02-SEP-2001  
ACCESSION AF358859  
VERSION AF358859.1 GI:15420534  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4  
receptor suggests substantial species variation  
JOURNAL Unpublished  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson  
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,  
CA 92121, USA

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AF358860				
LOCUS				
DEFINITION Rattus norvegicus histamine H4 receptor mRNA, complete cds.				
ACCESSION AF358860				
VERSION AF358860.1 GI:15420536				
KEYWORDS				
SOURCE Rattus norvegicus (Norway rat)				
ORGANISM Rattus norvegicus				
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Rattus.				
REFERENCE 1 (bases 1 to 1593)				
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.				
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation				
JOURNAL Unpublished				
REFERENCE 2 (bases 1 to 1593)				
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.				
TITLE Direct Submission				
JOURNAL Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA				
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BC111862

LOCUS  
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ACCESSION  
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REFERENCE  
AUTHORS  
CONSTRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
CONSTRM  
TITLE  
JOURNAL  
REMARK  
COMMENT

BC111862 1308 bp mRNA linear ROD 16-JAN-2006  
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IMAGE:40046148), complete cds.  
BC111862  
BC111862.1 GI:84993254  
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Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1308)  
Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Shat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hele, F.,  
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J.,  
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smailus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Mammalian Gene Collection Program Team  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1308)  
NIH MGC Project  
Direct Submission  
Submitted (13-JAN-2006) National Institutes of Health, Mammalian  
Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Baylor Human Genome Sequencing Center  
cDNA Library Preparation: Baylor Human Genome Sequencing Center  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUMI)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akhtar, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hagnighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
Maddipati, K.R., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILLUMI at: <http://image.llnl.gov>  
Series: IRAM Plate: 15 Row: c Column: 19.

FEATURES  
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TCCAGTGCCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT

DB 556

Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
----- Project Information -----



Center project name: M BA0314O21

## FEATURES

**source**

Location/Qualifiers

1. 199837

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QY	598	TACTGGAGCGTGTGGAAGCGTAGGGCTCTCAGTAGTGCCCTAGCCATCTGCGATTCTTCC	657	
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## RESULTS

REF ID: A2850

SLUG  
LOCITY

LOCUS IDENTIFICATION

COLSSEJQ  
TINTJED

ACCESSION  
VERSION

## KEYWORDS

**KEYWORDS**  
**SOURCE**

ORGANIZATION

11

## REFERENCES

**AUTHOR:**

**TITLE**

**JOURNAL:**

## FEATURES

**nos:**

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Query Match	58.4%;	Score 686.6;	DB 2;	Length 1173;
Best Local Similarity	75.1%;	Pred. No. 4.1e-225;		
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 ACCESSION CS173186  
 VERSION CS173186.1 GI:77153219  
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 REFERENCE  
 AUTHORS Chen, R.  
 TITLE Human Orphan G Protein-Coupled Receptors  
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 Arena Pharmaceuticals, Inc. (US)  
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 Best Local Similarity 75.1%; Pred. No. 4.1e-225;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
  
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 DEFINITION Sequence 13 from Patent EP1584683.  
 ACCESSION CS178018  
 VERSION CS178018.1 GI:77733617  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
  
 REFERENCE  
 AUTHORS Chen, R.  
 TITLE Human orphan g protein-coupled receptors  
 JOURNAL Patent: EP 1584683-A 13 12-OCT-2005;  
 Arena Pharmaceuticals, Inc. (US)  
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Best Local Similarity 75.1%; Pred. No. 4.1e-225;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCTTGGCAATTT 60
DB 1 ATGCCAGATATAATAGCACAAATTAATATCACTAAGCACTCGTGTTAGCATTT 60
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DEFINITION   Sequence 1 from patent US 6613533.
ACCESSION    AR391860
VERSION      AR391860.1 GI:40115588
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 1173)
AUTHORS      Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,
              Umland, S.P. and Wang, S.
TITLE        Histamine receptor
JOURNAL      Patent: US 6613533-A 1 02-SEP-2003;
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Query Match      58.4%; Score 686.6; DB 2; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.1e-225;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCTTGGCAATTT 60
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ACCESSION            AX109119
VERSION              AX109119.1  GI:13924093
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SOURCE               Homo sapiens
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REFERENCE
AUTHORS              Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,
                     Umland, S. and Wang, S.
TITLE                Histamine receptor
JOURNAL              Patent: WO 0125432-A 1 12-APR-2001;
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Best Local Similarity 75.1%;   Pred. No. 4.1e-225;
Matches 886;   Conservative 0;   Mismatches 284;   Indels 9;   Gaps 2;
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RESULT 11  
AX139113  
LOCUS AX139113 1173 bp DNA linear PAT 30-MAY-2001  
DEFINITION Sequence 1 from Patent EP1096009.  
ACCESSION AX139113  
VERSION AX139113.1 GI:14274791  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
1 Peter, B. and O'Reilly, M.A.  
G-protein coupled receptor-like polypeptide  
TITLE Patent: EP 1096009-A 1 02-MAY-2001;  
JOURNAL Pfizer Limited (GB) ; PFIZER INC. (US)  
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Best Local Similarity 75.1%; Pred. No. 4.1e-225;  
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Qy 1 ATGTCGAGTCTAACAGTACTGGCATCTGCCACAGCTGCTCAGNCCCTTGGCATTT 60  
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LOCUS AF325356 1173 bp mRNA linear PRI 11-SEP-2001  
DEFINITION Homo sapiens histamine receptor H4 (AXOR35) mRNA, complete cds.  
ACCESSION AF325356  
VERSION AF325356.1 GI:15553202  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Hominidae; Homo.  
1 (bases 1 to 1173)  
Zhu, Y., Michalovich, D., Wu, H.-L., Tan, K.B., Dytko, G.M.,  
Mannan, I.J., Boyce, R., Alston, J., Tierney, L.A., Li, X.,  
Herrity, N.C., Vawter, L., Sarau, H.M., Ames, R.S., Davenport, C.M.,  
Hieble, P., Wilson, S., Bergsma, D.J. and Fitzgerald, L.R.  
Cloning, expression, and pharmacological characterization of a  
novel human histamine receptor  
JOURNAL Mol. Pharmacol. 59 (3), 434-441 (2001)  
PUBMED 11179436

REFERENCE 2 (bases 1 to 1173)  
AUTHORS Zhu, Y., Michalovich, D. and Fitzgerald, L.R.  
TITLE Direct Submission  
JOURNAL Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd., PO Box 1539, King of Prussia, PA 19406, USA  
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Query Match 58.4%; Score 686.6; DB 5; Length 1173;  
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QY 1 ATGTCGGAGCTAACAGTACTGGGATCTTCCACCAGCTCTCAGGTCCTTGGCAATTT 60  
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DEFINITION Homo sapiens histamine receptor H4 mRNA, complete cds.  
ACCESSION AF329449  
VERSION AF329449.1 GI:13876643  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1173)  
AUTHORS Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,  
Anthes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N.,  
Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.  
and Monsma, F.J. Jr.  
TITLE Cloning and characterization of a novel human histamine receptor  
JOURNAL J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)  
PUBMED 11181941  
REFERENCE 2 (bases 1 to 1173)  
AUTHORS Monsma, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and  
Bayne, M.  
TITLE Direct Submission  
JOURNAL Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough  
Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,  
USA  
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Query Match		58.4%; Score 686.6; DB 5; Length 1173;	
Best Local Similarity		75.1%; Pred. No. 4.1e-225;	
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;			
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/db_xref="GI:113876644"			
Discovery of a novel member of the histamine receptor family			
Mol. Pharmacol. 59 (3), 427-433 (2001)			
11179435			
2 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens (human)			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
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Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
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O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
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Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
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O'Dowd, B.F.			
Homo sapiens			
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Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
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Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
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Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
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Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Homo sapiens			
1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D			







GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 19:08:42 ; Search time 755 Seconds  
(without alignments)  
10860.085 Million cell updates/sec

Title: US-10-626-445-5  
Perfect score: 1176  
Sequence: 1 atgtcgagctcaacagctac.....accagtcagtcattctttgga 1176

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8.\*

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- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1176	100.0	1176	6	AAI70981
2	1176	100.0	1538	12	ADO30257 Mouse GPC
3	958.4	81.5	1176	6	AAI70982 Rat hist
4	686.6	58.4	1173	3	AAA46023 Human G p
5	686.6	58.4	1173	3	AAO01124 Human orp
6	686.6	58.4	1173	4	AAI83203 Human GPC
7	686.6	58.4	1173	5	AAH24007 Human G p
8	686.6	58.4	1173	6	ABZ80663 Human his
9	686.6	58.4	1173	6	ABQ78739 Nucleotid
10	686.6	58.4	1173	6	AAI70980 Human his
11	686.6	58.4	1173	8	ACA93262 Human cdn
12	686.6	58.4	1173	10	ADG98759 Human orp
13	686.6	58.4	1173	10	ABS57063 Human cdn
14	686.6	58.4	1173	11	ADJ26922 Human end
15	686.6	58.4	1173	12	ADG86374 Human end
16	686.6	58.4	1173	12	ADJ88375 Novel hum
17	686.6	58.4	1173	12	ADP20167 Human G p
18	686.6	58.4	1173	12	ADQ75073 Human cdn

19	686.6	58.4	1173	14	ADVA3700
20	686.6	58.4	1173	14	ADY86899
21	686.6	58.4	1266	6	ABK12959 DNA seque
22	686.6	58.4	1300	6	ABA02496 Human G p
23	686.6	58.4	1312	4	AAH47911 Human G p
24	686.6	58.4	3689	8	ABZ42573 Human his
25	686.6	58.4	3689	12	ADO05719
26	686.6	58.4	3689	12	ADO29967
27	685.2	58.3	1170	9	AAAD55126
28	685	58.2	1227	4	AAAI66009
29	685	58.2	1265	6	AAE98078 Human GPR
30	685	58.2	1265	6	AAE98078 Human DNA
31	683.4	58.1	1173	6	AAI67750 Human his
32	613	52.1	1170	6	AAI70983
33	505.8	43.0	1166	9	AAAD55124
34	436.6	37.1	1103	9	AAAD55123
35	371	31.5	1950	13	ADU82889
36	271.6	23.1	1326	6	AAAD37667
37	269	22.9	540	6	AAE98150
38	172.8	14.7	1239	2	AAE84570
39	172.8	14.7	1239	3	AAA70639
40	172.8	14.7	2700	2	AAE84571
41	172.8	14.7	2700	3	AAA70640
42	171.6	14.6	1311	9	AAI59979
43	168.6	14.3	1203	9	AAI59985
44	145.4	12.4	1338	12	ADF66834
45	145.4	12.4	18105	8	ABZ82337

ALIGNMENTS

RESULT 1

AAI70981  
ID AAI70981 standard; cdna; 1176 BP.

XX AAI70981;

XX 18-MAR-2002 (first entry)

XX Mouse histamine H4 receptor cDNA.

XX Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
XX antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
XX diagnosis; gene therapy; ss.

XX Mus musculus.

XX WO200192485-A1.

XX 06-DEC-2001.

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WFI; 2002-114339/15.

XX P-PSDB; AAM50565.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
XX the proteins, useful in gene therapy for treating diseases where it is  
XX beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 4; Fig 5A; 92pp; English.

XX The present sequence is that of a cDNA clone encoding a murine histamine  
XX receptor of the H4 subtype. The cDNA was isolated from a mouse spleen  
XX cDNA library. It shows 72.8% homology to the human H4 receptor coding  
XX region. The invention provides mammalian (human, mouse, rat and guinea

CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
CC useful for diagnosing, treating or preventing asthma, allergy,  
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
CC disorders of the neuroendocrine system, stress and spasticity  
CC  
SQ Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

Db	781	ATCCTGGTGCTCTTAAGGACTC	AATGAGCAGCAGGATATCA	CTCGCTTCAAAAGTGGGTTC	840
Qy	841	TTCTGGCGATCGAAAGTGCAGCGCTTCG	CCAAAGGAGGAGTACG	CAGAGCTTCTCAGAGGC	900
Db	841	TTCTGGCGATCGAAAGTGCAGCGCTTCG	CCAAAGGAGGAGTACG	CAGAGCTTCTCAGAGGC	900
Qy	901	AGGAAGCTACGCCAGGTCACTGGCCATCCT	TCTCAGCGCTTTTGCCATTTGCTGGGTCCA	960	
Db	901	AGGAAGCTACGCCAGGTCACTGGCCATCCT	TCTCAGCGCTTTTGCCATTTGCTGGGTCCA	960	
Qy	961	TACTGTCTGTTCACAATTGTGCTTTCAATT	ATCCCGACGAAACGCCCAAAATCGGTG	1020	
Db	961	TACTGTCTGTTCACAATTGTGCTTTCAATT	ATCCCGACGAAACGCCCAAAATCGGTG	1020	
Qy	1021	TGGTACAGCAATTCGCTTCGCGTCGAATG	GTTCAAATTCGTTTAAATCCCTTTCTGTAC	1080	
Db	1021	TGGTACAGCAATTCGCTTCGCGTCGAATG	GTTCAAATTCGTTTAAATCCCTTTCTGTAC	1080	
Qy	1081	CCTTTGTGTGCACAGGCGTTTCCAGAAGCT	TTTCTGGAAGATACTTTGTGTGACAAAGCAA	1140	
Db	1081	CCTTTGTGTGCACAGGCGTTTCCAGAAGCT	TTTCTGGAAGATACTTTGTGTGACAAAGCAA	1140	
Qy	1141	CCAGCGCTGTGCACAGAACCAAGTCAGTAT	CTTCTTGA	1176	
Db	1141	CCAGCGCTGTGCACAGAACCAAGTCAGTAT	CTTCTTGA	1176	

RESULT 2  
ADO30257  
ID ADO30257 standard; cdna; 1538 BP.

PT Novel mammalian G protein coupled receptors, useful for identifying

PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
XX  
PS  
XX Claim 151; SEQ ID NO 1360; 542pp; English.  
XX  
CC The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridize to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
CC nucleic acid of the invention. Note: The full sequence data for this  
CC patent did not form part of the printed specification; those sequences  
CC not shown were obtained in electronic format directly from WIPD at  
CC ftp.wipo.int/pub/published\_pt\_sequences.  
XX  
SQ Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1176; DB 12; Length 1538;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAAGCTGCTCAGTGCCCTTGGCATTT 60  
DB 61 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAAGCTGCTCAGTGCCCTTGGCATTT 120  
QY 61 TTAATGCTCTCATTTGCCCTTGTCTAATAGGTAGGCAATGCTGTGTCATCTTAGCCTTT 120  
DB 121 TTAATGCTCTCATTTGCCCTTGTCTAATAGGTAGGCAATGCTGTGTCATCTTAGCCTTT 180  
QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180  
DB 181 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 240  
QY 181 GACTTCCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG 240  
DB 241 GACTTCCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG 300  
QY 241 AATTTTGGAGTGGATCTGCATGTTTGGCTCATTTACTGACTATCTTTGTGCACCGCA 300  
DB 301 AATTTTGGAGTGGATCTGCATGTTTGGCTCATTTACTGACTATCTTTGTGCACCGCA 360  
QY 301 TCTGTCTACAATATTGTCCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAAATGCTGTG 360  
DB 361 TCTGTCTACAATATTGTCCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAAATGCTGTG 420  
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTGG 420  
DB 421 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTGG 480  
QY 421 ATACTGGCTTTCTTGTGAATGGCCCGATGATTTCTGGCTTCAGATTCTTGGGAAGACAGC 480

DB 481 ATACTGGCTTTCTTGTGAATGGCCCGATGATTTCTGGCTTCAGATTCTTGGGAAGACAGC 540  
QY 481 ACGAACACAAAGAGCATGTGAGCCTTGGCTTTGTTTACAGAGTGGTACATCCTCACCATTACA 540  
DB 541 ACGAACACAAAGAGCATGTGAGCCTTGGCTTTGTTTACAGAGTGGTACATCCTCACCATTACA 600  
QY 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600  
DB 601 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 660  
QY 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGTGGCCCTAGCCATGCTGATCTTCCACT 660  
DB 661 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGTGGCCCTAGCCATGCTGATCTTCCACT 720  
QY 661 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTCAGGACAAGTAAT 720  
DB 721 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTCAGGACAAGTAAT 780  
QY 721 CCTGGATTGAGGAATCAGCTGCTCATCTGCTCCTCAGAAAGTCTCGAAGAAAGACAGC 780  
DB 781 CCTGGATTGAGGAATCAGCTGCTCATCTGCTCCTCAGAAAGTCTCGAAGAAAGACAGC 840  
QY 781 ATCTGTGTGCTCTTAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 840  
DB 841 ATCTGTGTGCTCTTAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 900  
QY 841 TTCTGCGATTCGGAAGTGCAGCGCTTCGCCAAGGGAGTACGACAGCTTCTCAGAGGC 900  
DB 901 TTCTGCGATTCGGAAGTGCAGCGCTTCGCCAAGGGAGTACGACAGCTTCTCAGAGGC 960  
QY 901 AGAAGCTAGCAGGCTCAGTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGCTCCA 960  
DB 961 AGAAGCTAGCAGGCTCAGTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGCTCCA 1020  
QY 961 TACTGTCTGTTCACAATTTGCTTCAACTTACCAGAAAGGAGTACGACAGCTTCTCAGAGGC 1020  
DB 1021 TACTGTCTGTTCACAATTTGCTTCAACTTACCAGAAAGGAGTACGACAGCTTCTCAGAGGC 1080  
QY 1021 TGGTACAGCATTTGCTTCTGGCTGCAATGGTTCATTTGTTTAAATCCCTTTCTGTAC 1080  
DB 1081 TGGTACAGCATTTGCTTCTGGCTGCAATGGTTCATTTGTTTAAATCCCTTTCTGTAC 1140  
QY 1081 CTTTGTGTACAGGCGTTTCCAGAAAGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140  
DB 1141 CTTTGTGTACAGGCGTTTCCAGAAAGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1200  
QY 1141 CCAGCGCTGTCCAGAACAGTCAGTATCTTCTTGA 1176  
DB 1201 CCAGCGCTGTCCAGAACAGTCAGTATCTTCTTGA 1236  
RESULT 3  
AAI70982  
ID AAI70982 standard; cDNA; 1176 BP.  
XX  
AC AAI70982;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Rat histamine H4 receptor cDNA.  
XX  
KW Histamine H4 receptor; rat; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
XX diagnosis; gene therapy; ss.  
OS Rattus rattus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.  
PR (ORTH ) ORTHO-MCNEIL PHARM INC.  
PA  
XX  
XX  
PI Lovenberg T, Liu C;  
XX  
XX WPI; 2002-114339/15.  
DR P-PSDB; AAM50566.  
XX  
XX  
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is  
PT beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
XX  
PS Claim 4; Fig 5C; 92pp; English.  
XX  
XX The present sequence is that of a cDNA clone encoding a rat histamine  
CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA  
CC library. It shows 72.5% homology to the human H4 receptor coding region.  
CC The invention provides mammalian (human, mouse, rat and guinea pig)  
CC histamine H4 receptor nucleic acid molecules (see AAL70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
CC useful for diagnosing, treating or preventing asthma, allergy,  
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
CC disorders of the neuroendocrine system, stress and spasticity  
XX  
SQ Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;

Query Match 81.5%; Score 958.4; DB 6; Length 1176;  
Best Local Similarity 88.4%; Pred. No. 2e-289;  
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGGCCAGCTGCTCAGTCCCTTGGCATTTT 60  
DB 1 ATGTGGAGTCTAACGGCACTGACGTCTTGGCACTGCTCAAGTCCCTTGGCATTTT 60  
QY 61 TTAATGCTTTCATTTGGCTTTTGTATTAATGTTAGGCAATGCTGGTCACTTAGCCCTTT 120  
DB 61 TTAATGCTTTCATTTGGCTTTTGTATTAATGTTAGGCAATGCTGGTCACTTAGCCCTTT 120  
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTC 180  
DB 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTC 180  
QY 181 GACTTCCTGGTGGTTTGATTTTCATTCCTCTGTGATACATCCCTCAGTGTGTTAACTGG 240  
DB 181 GACTTCCTGGTGGTGTGATCTCCATCTCTGTATACATCCCTCAGTGTGTTAACTGG 240  
QY 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCATTAATCTGATCTATCTTTGTGCACGCA 300  
DB 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCATTAATCTGATCTATCTTTGTGCACGCA 300  
QY 301 TCTGCTCACAATATGTCCCTCATTAGCTAGCTAGTACGATCAGTGTTCATAATGCTGTG 360  
DB 301 TCGGCTCAGATATTGTCCCTCATTAGCTAGCTAGTACGATCAGTGTTCATAATGCTGTG 360  
QY 361 TCTTATAGGCTCAACACATCGGATCATGAAGATTGTTGCTCAATGGTGGCTGTTTGG 420  
DB 361 CGTTATAGACACAGCACACTGGCATCTTGAATAATTTGTTGCTCAATGGTGGCTGTTTGG 420  
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QY 481 ACNAACAACAAGGACTGTGAGCCCTGGCTTTGTATACAGATGGTATCCTCACCATTACA 540

DB 481 ACCAACACAGAGAGTGCAGACCTGGCTTTGTATCTGAGTGGTACATCTCGCCATTACA 540  
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QY 661 ACCTTCTCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720  
DB 661 ACCTTCTCAGGCGCACTGGACACTCAGCAGAACTGGGTGGCTTGGCTTGTAGGACAAAGTCTT 720  
QY 721 CCTGGATTGAAGAAATCAGCTGCATCTCGTCACTCAGAAAGTCTCGAAAGAAAGCAGC 780  
DB 721 CCTGGATTGAAGAAATCAGCGCATCTCTTCAATTCAGAAAGTCCACGAGAAAGAGCAGT 780  
QY 781 ATCTGTGTCTTAAAGGACTCAGTGAACAGCAGATATCATCTGCTTCAAAGTGGGTTC 840  
DB 781 CTCTGTGTCTTAAAGGACTCAGTGAACAGCAGTATCATCTGCTTCAAAGTGGGTTC 840  
QY 841 TTCTGGCATCGGAAGTGTGAGCGCTTTCGCCAAGGGAGTACGAGAGCTTCTCAGAGGC 900  
DB 841 TTCTGGCATCGGAAGCGCCAGTCTTCCACAGAGAGCAGCGTGGAGCTTCTCAGAGGC 900  
QY 901 AGAAGCTAGCAGGTCACTGGCCATCTTCTCAGGCTTTTGCATTTCTCGTGGCTCCA 960  
DB 901 AGAAGCTAGCAGGTCTGCTGGCTGCAATGGTTCAATTCGTTTGTATTCCTTCTGTAC 1080  
QY 961 TACTGTCTGTTCACAAATGTCTTCAACTTACCCAGAACCGAACCCCAATCGGTG 1020  
DB 961 TATTGCTCTTCAAAATGTCTTCAACTTATTCGACAGGGAGCGCCCAATCGATT 1020  
QY 1021 TGTACAGCATTTGCTTCTGGCTGCAATGGTTCAATTCGTTTGTATTCCTTCTGTAC 1080  
DB 1021 TGTGTACAGCATAGCTTCTTGGCTACAGTGGTTCAATTCACCTTATTAATTCCTTCTATAC 1080  
QY 1081 CCTTTGTGCACAGGCTTTTCCAGAAAGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140  
DB 1081 CCTTTGTGCACAGAGCTTTTCCAGAAAGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140  
QY 1141 CCAGCGCTGTGCAGAACCAAGTCAAGTATCTTCTTGA 1176  
DB 1141 CCAGCACCTTCACAGACCCAGTCAAGTATCTTCTTGA 1176

RESULT 4  
AAA46023  
ID AAA46023 standard; cDNA; 1173 BP.  
XX  
AC AAA46023;  
XX  
DT 22-AUG-2000 (first entry)  
XX  
DE Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.  
XX  
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;  
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
XX ss.  
OS Homo sapiens.  
XX  
XX WO200022131-A2.  
XX  
PD 20-APR-2000.  
XX  
PF 13-OCT-1999; 99WO-US024065.  
XX  
PR 13-OCT-1998; 98US-00170496.  
PR 12-NOV-1998; 98US-0108029P.  
PR 20-NOV-1998; 98US-0109213P.  
PR 27-NOV-1998; 98US-0110060P.

PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123944P.  
 PR 12-MAR-1999; 99US-0123945P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123948P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 12-MAR-1999; 99US-0123951P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 28-MAY-1999; 99US-0137567P.  
 PR 28-JUN-1999; 99US-0141448P.  
 PR 27-AUG-1999; 99US-0151114P.  
 PR 03-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX  
 PI Behan DP, Lehmann-Bruinema K, Chalmers DT, Chen R, Dang HT;  
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
 XX  
 DR WPI; 2000-317986/27.  
 DR P-PSDB; AAB02831.  
 XX  
 PT Non-endogenous, human G protein-coupled receptors for screening receptor,  
 PT inverse or partial agonists useful as therapeutic agents.  
 XX  
 PS Example 1; Page 88-89; 187pp; English.  
 CC The present invention describes transmembrane receptors, preferably human  
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is  
 CC unknown (orphan GPCR receptors). More specifically the present invention  
 CC relates to non-endogenous, constitutively activated versions of a human  
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
 CC identification of candidate compounds as receptors agonists, inverse  
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 58.4%; Score 686.6; DB 3; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 4e-204;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
 QY 1 ATGTCCGAGTCTAACAGTACTGCGCACTTCCACCAGCTGCTCAGGTCCCTTGGCATTT 60  
 DB 1 ATGCCAGACTACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
 QY 61 TTAATGCTTCATTTGCTTTGTCTATAATGGTAGGCAATGCTGGTGCATCTTAGCCTTT 120  
 DB 61 TTTATGCTCTAGTCTTTTGTCTATAATGCTAGGAATGCTTTGGTTCATTTTAGCTTTT 120  
 QY 121 GTGGTGCAGAAACCTTAGACATCGAAGTAATTTTTTCTTAATTTGGCTATTTCT 180  
 DB 121 GTGGTGCAGAAACCTTAGACATCGAAGTAGTATTTTTTCTTAATTTGGCCTCTCT 180  
 QY 181 GACTTCTCGTGGTGTGATTTCATCTCTCTACATCCCTCAGGTGTTGTTAACTGG 240  
 DB 181 GACTTCTTTGTGGGTGTGATCTCCATTTCTTTGTATATCCCTCACACGCTGTTTCAATGG 240

QY 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGCTCATTTACTGACTATCTTTTGTGTCACCGCA 300  
 DB 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTTTTGTATGTACAGCA 300  
 QY 301 TCTGTCTACAAATATTGTCTCTCATTAGCTACGATCGATACAGTCAGTTCAGATTTCAAAATGCTGTG 360  
 DB 301 TCTGTATATAACATTTGCTCTCCTCAGCTATGATGATACCTGTCAGTCTCAATGCTGTG 360  
 QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTTTTGG 420  
 DB 361 TCTTATAGAACTCAACATACTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCGGTTTGG 420  
 QY 421 ATACTGGCTTTCTTGTGAATGAGCCGATCTCTGCTGCTTCAATTTGCTCAAAATGGTGGCTTTTGG 480  
 DB 421 GTGCTGGCCCTTCTTGTAGTGAATGGGCCAATGATTCTAGTTTTCAGAGTCTTGGGAAGGA---- 476  
 QY 481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTACAGAGTGGTACATCTCCACCATTTACA 540  
 DB 477 --TGAAGGTAGTGAATGTGAACCTTGAATTTTTTCGGAATGGTACATCTCTTGGCCATACA 534  
 QY 541 ATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGTGGCTTATTTCAATGTACAGATTTCAC 600  
 DB 535 TCATTCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATCAATATTTAT 594  
 QY 601 TGAAGCCTGTGGAAGCGTAGGGCTCTCAGTAGTGCCCTAGCCATGCTGGAATTTCTCCACT 660  
 DB 595 TGGAGCCTGTGGAAGCGTGTATCATCTCAGTAGGTGCCAAAGCCATCTCGGACTGACTGCT 654  
 QY 661 ACCTCTTCCAGTGTCTTCAGGACACTTACACAGAGCTGGGGTGGCTTCAGGACCAAGTAAT 720  
 DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714  
 QY 721 CTGGAATTGAAGGAATCAGCTGCATCTCGTCACCTCAGAAAAGTCTCTCGAAAGAAAGAGCAGC 780  
 DB 715 TCTGCATCGACAGAAGTTCTGTCATCTTTTCATTTCAGAGAGACAGAGAGAGAGTAGT 774  
 QY 781 ATCTGTGTGCTTAAAGGACTCATGAACAGCAGATATCATCTGCTTCAAAAGTGGTTC 840  
 DB 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834  
 QY 841 TTCTGGCGATCGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGACAGCTTCTCAGAGGC 900  
 DB 835 TTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAAACATGTTGAACCTGCTTAGAGGC 894  
 QY 901 AGGAAGCTAGCCAGGCTCAGTGGCCATCTTCTCAGAGCGCTTTTGCATTTTCTGGGCTCCA 960  
 DB 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGGTTTTTGTGTTGCTGGGCTCCA 954  
 QY 961 TACTGTCTGTTCACAAATTTGCTTTTCAACTTACCCAGAACGGAAGCCCCCAATTCGGTG 1020  
 DB 955 TATTTCTGTTCACAAATTTGCTTTTCAATTTTATTTCTCAGCAACAGGTCCTAAATCAGTT 1014  
 QY 1021 TGTACAGCATTTGCCCTTCTGGCTGCAATGGTTCATTCGTTTGTATCTTCTTCTGTATC 1080  
 DB 1015 TGTGTAGAAATTTGCTTTTGGCTTTCAGTGGTTCATTTCTTCTTCTTCTTCTTCTTGTAT 1074  
 QY 1081 CCTTTGTGTACAGGCGTTTTCAGAAAGGCTTTCTGGAAGACTCTTGTGTGACAAAGCAA 1140  
 DB 1075 CCATTGTGTACAGGCGCTTTTCAAAAGGCTTTTCTGAAATATTTTTGTATATAAAGCAA 1134  
 QY 1141 CCAGCGCTGTGCAGAAC---CAGTCAGTATCTTCTTGA 1176  
 DB 1135 CCTCTACCATCAACACACAGTCGGTTCAGTATCTTCTTAA 1173

RESULT 5

AAD01124

ID AAD01124 standard; cDNA; 1173 BP.

XX

AC AAD01124;

XX

DT 02-NOV-2000 (first entry)

XX Human orphan G protein-coupled receptor hrUP7 cDNA.  
DE  
XX  
XX Human; orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;  
KW transmembrane receptor; signal cascade; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1173  
FT *1*.1173  
FT */\*tag= a*  
FT */product= "hrUP7"*  
FT */note= "Human orphan G protein-coupled receptor"*  
XX  
PN WO200031258-A2.  
XX  
XX  
XX 02-JUN-2000.  
XX  
XX 13-OCT-1999; 99WO-US023687.  
XX  
XX 20-NOV-1998; 98US-0109213P.  
XX 16-FEB-1999; 99US-0120416P.  
XX 26-FEB-1999; 99US-0121852P.  
XX 12-MAR-1999; 99US-0123946P.  
XX 12-MAR-1999; 99US-0123949P.  
XX 28-MAY-1999; 99US-0136436P.  
XX 28-MAY-1999; 99US-0136437P.  
XX 28-MAY-1999; 99US-0136439P.  
XX 28-MAY-1999; 99US-0136567P.  
XX 28-MAY-1999; 99US-0137127P.  
XX 28-MAY-1999; 99US-0137131P.  
XX 29-JUN-1999; 99US-0141448P.  
XX 29-SEP-1999; 99US-0156555P.  
XX 29-SEP-1999; 99US-0156633P.  
XX 29-SEP-1999; 99US-0156634P.  
XX 29-SEP-1999; 99US-0156653P.  
XX 01-OCT-1999; 99US-0157280P.  
XX 01-OCT-1999; 99US-0157281P.  
XX 01-OCT-1999; 99US-0157282P.  
XX 01-OCT-1999; 99US-0157293P.  
XX 01-OCT-1999; 99US-0157294P.  
XX 12-OCT-1999; 99US-00416760.  
XX 12-OCT-1999; 99US-00417044.  
XX  
XX (AREN-) ARENA PHARM INC.  
XX  
XX  
XX Chen R, Dang HT, Liaw CW, Lin I;  
XX  
XX WPI; 2000-400068/34.  
XX P-PSDB; AAY71297.  
XX  
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs for  
XX use in the identification of G protein-coupled receptor agonists.  
XX  
XX Claim 25; Page 59; 102pp; English.  
XX  
XX The present sequence is a cDNA encoding hrUP7, an endogenous human orphan  
XX G protein-coupled receptor (GPCR). The full length hrUP7 cDNA was cloned  
XX by RT-PCR using human peripheral leucocyte cDNA as template. The orphan  
XX GPCR of the invention, like all GPCRs has seven transmembrane alpha  
XX helices with an extracellular N-terminus and an intracellular C-terminus.  
XX However, no endogenous ligands has yet been identified for the proteins  
XX of the invention. The orphan GPCRs may be used in the identification of  
XX their endogenous ligands, and to screen potential GPCR agonists and  
XX antagonists for use as pharmaceutical agents. The proteins may also be  
XX used in the study of GPCR-mediated signalling cascades, and to elucidate  
XX their precise role in normal and diseased human conditions. Nucleic acid  
XX encoding human orphan GPCRs may be used for tissue localisation  
XX expression analysis to provide information about their function in  
XX healthy and pathological states  
XX  
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 3; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 4e-204;  
Matches 885; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
QY 1 ATGTGGAGTCTAACAGTACTTGGCATCTTGCACACCAGCTGCTCAGGTCCTTGGCAATTT 60  
DB 1 ATGCCAGATACTAATAGACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60  
QY 61 TTAATGCTCTTCATTTGCCTTTGCTATAAATGGTAGGCAATCTGTGGTCATCTTAGCCCTTT 120  
DB 61 TTTATGCTCTTAGTAGCTTTTGTCTATAAATCTAGGAATGCTTTGGTCATTTTAGCTTTT 120  
QY 121 GTGGTGACAGAAAACCTTAGACATCGAAGTAATTTATTTTTTCTTAATTTGGCTATTCT 180  
DB 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTTTCTTAATTTGGCCATCTCT 180  
QY 181 GACTTCCTCTGGGTTTGATTTCCATTCCTCTGTATACATCCCTCAGTGTGTTTAACTGG 240  
DB 181 GACTTCCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTTCSAATGG 240  
QY 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300  
DB 241 GATTTTGGAAAGAAATCTGTGTAATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300  
QY 301 TCTGTCTACAAATATTTGTCTCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAAATGCTGTG 360  
DB 301 TCTGTATATAACATTTGTCTCTCATCAGCTATGATCGATACCTGTCCAGTCTCAAAATGCTGTG 360  
QY 361 TCTTATAGGCTCAACACACATCGGCAATCATGAAGATTTGCTCTCAATTTGGTGGCTGTTTGG 420  
DB 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTTGTTACTCTGTAGTGGTGGCGGTTTGG 420  
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480  
DB 421 GTGCTGGCTTTCTTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGAAGAGA --- 476  
QY 481 ACGAAACAAAGGACTGTGAGCCTGGCTTTGTGTACAGAGTGGTACATCTCCATTTACA 540  
DB 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATACATCTTGGCATCACA 534  
QY 541 ATGCTCTTGGAAATTCCTGTCTCTGTGTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600  
DB 535 TCATTTCTTGAATTCGTGATCCCAAGTCAUCTTAGTTCGCTTATTTTCAACATGAATATTAT 594  
QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGTGCCCTAGCCATGCTGGATTTCTCCACT 660  
DB 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGTGCCAAAGCCATCTGCACTGACTGCT 654  
QY 661 ACCTCTTCCAGTGTCTTCAAGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720  
DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
QY 721 CTGTGATTAAGGAATCAGCTGCAATCTGTCATCTCAGAAAGTCTCTGAAAGAAAGAGCAGC 780  
DB 715 TCTGCATCGACAGAAAGTTCTTGCATCTCTTCAATTCAGAGAGACAGAGGAGAGAGTAGT 774  
QY 781 ATCTGTGTGCTTAAAGGACTCATCAACAGACAGATATCACTGCTTCAAAGTGGTTC 840  
DB 775 CTCATGTTTTTCCCTCAAGAAACAAGATGAATAGCAATACAATTTGTTCCAAATGGTTC 834  
QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGGC 900  
DB 835 TTCTCCCAATCAGATTTCTGTAGCTTTTCCAAAGGGAACATGTTGAATGCTTTAGAGCC 894  
QY 901 AGGAAGCTAGCAGGTCACTGGCCATCTTCTGTAGCCGCTTTTGCATTTTGTGGGCTCCA 960  
DB 895 AGGAGATTAGCAAGTCACTGGCCATTTCTTTAGGGGTTTTTGTGTTTGTGTGGGCTCCA 954  
QY 961 TACTGTCTGTTCAAATTTGCTTTCATTTTACCTTACCCAGAACGGAACGCCCAATCGGTG 1020  
DB 955 TATTCTCTGTTCAAATTTGCTTTCATTTTATTTCTCAGCAACAGGTCCTTAATTCAGTT 1014  
QY 1021 TGGTACAGCATTTGCCCTTCTGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTTCTGTGAC 1080



Db 1015 TGGTATAGATTGCAATTTGGCTTCAGTGGTTCAATTCCTTTGTCATCTCTTTGTAT 1074  
 Qy 1081 CCTTTGTGCACAGCGCTTCCAGAGCGCTTCTGGAAGATACATTTGTGTGACAAAGCAA 1140  
 Db 1075 CCATTGTGTGCACAGCGCTTCCAGAGCGCTTCTGGAAGATATTTGTATATAAAGCAA 1134  
 Qy 1141 CCAGCGGTGTCACAGAAC--CAGTCAGTATCTCTTGA 1176  
 Db 1135 CCTCTACATCAACAACAGTCGGTCAGTATCTCTTAA 1173

## RESULT 6

AAF83203

ID AAF83203 standard; cDNA; 1173 BP.

XX AC

XX AAF83203;

XX XX

DT 09-JUL-2001 (first entry)

XX XX

XX Human GPCR-like polypeptide, PFI-013 encoding cDNA.

XX XX

G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;  
 antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;  
 osteopathic; neuroprotective; nootropic; dermatological; gynecological;  
 signal transduction; ss.

XX XX

OS Homo sapiens.

XX XX

FH Key Location/Qualifiers

CDS 1..1173

FT /\*tag= a

FT /product= "PFI-013"

XX XX

PN EP1096009-A1.

XX XX

PD 02-MAY-2001.

XX XX

PF 24-OCT-2000; 2000EP-00309364.

XX XX

PR 29-OCT-1999; 99GB-00025641.

XX XX

PR 20-APR-2000; 2000GB-00009973.

XX XX

(PFI2 ) PFIZER LTD.

PA PA

(PFI2 ) PFIZER INC.

XX XX

PI Peter B, O'reilly MA;

XX XX

WPI; 2001-309854/33.

DR DR

P-PSDB; AAB62445.

XX XX

New G-protein coupled receptor-like polypeptide, polynucleotide for  
 screening drug candidates for treating diseases associated with signal  
 transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.

XX PS

Claim 1; Page 43; 66pp; English.

XX CC

This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor  
 (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be  
 expressed by standard recombinant methodology. Antibodies and modulators  
 of PFI-013 are useful in the manufacture of a medicament for treating  
 allergic disorder, including extrinsic asthma, immunological disorders,  
 such as intrinsic asthma, vasculitic granulomatous disease, interstitial  
 and other pulmonary disease, including chronic obstructive pulmonary  
 disease (COPD), infectious, inflammatory disease, such as inflammatory  
 bowel disease and neoplastic and myeloproliferative diseases. They are  
 also useful for treating obesity, diabetes, metabolic, neurological  
 diseases, psychotherapeutics, urogenital disease, reproduction and sexual  
 medicine, inflammation, cancer, tissue repair, dermatology, photoaging,  
 skin pigmentation, osteoporosis, cardiovascular, gastrointestinal  
 diseases, allergy and respiratory disease, sensory organ disorders, sleep  
 disorders and hair loss. The PFI-013 protein and nucleic acid are useful  
 in the diagnosis and treatment of the above conditions and also for

CC screening drug candidates for the treatment of diseases associated with  
 CC signal transduction. The antibodies are also useful for enrichment of  
 CC eosinophils from mammalian, especially human blood and for detecting the  
 CC protein in biological samples

XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.48; Score 686.6; DB 4; Length 1173;

Best Local Similarity 75.1%; Pred. No. 4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCATTTT 60

Db 1 ATGCCAGATACATAGCACAAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60

Qy 61 TTAATGTCCTTCAATTTGCTTTGTATTAATGGTAGGCAATGCTGTGGTCACTTTAGCCCTTT 120

Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATTAATGCTAGGAAATGCTTTGGTCACTTTAGCTTTT 120

Qy 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTCT 180

Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCTATTCT 180

Qy 181 GACTTCCTCGTGGTGTGATTTTCATTCCTCTGTACATCCCTCAGGTGTGTTTAACTGG 240

Db 181 GACTTCCTCGTGGTGTGATTTTCATTCCTCTGTACATCCCTCAGGTGTGTTTAACTGG 240

Qy 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCAATTAATGCTGTGTCACCGCA 300

Db 241 GAATTTTGGAAAGGAAATCTGTATTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300

Qy 301 TCTGTCTACAATATTGTCCTCATTAGCTACATGATACCACTCAGTTCAGTTCAGTGTG 360

Db 301 TCTGTATATAACATTTGTCCTCATCAGCTATGATGATGATGATGATGATGATGATG 360

Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTGCTCAATGGTGGCTGTTTG 420

Db 361 TCTTATAGAACTCAACATCTGSGGCTTGAAGATTGTTACTGTGATGGTGGCTGTTTG 420

Qy 421 ATACTGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAAGACGC 480

Db 421 GTGCTGCTCTTCTTAGTGAATGGCCCAATGATTCTAGTTCAGAGTCTTGGAAAGGA--- 476

Qy 481 ACGAAACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACA 540

Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534

Qy 541 ATGCTCTTGGAAATTCCTGCTTCCTGCTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600

Db 535 TCAATCTTGGAAATTCCTGCTTCCTGCTCATCTCTGTGGCTTATTTCAATGTACAGATTAT 594

Qy 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCGCTTAGCCATGCTGGATTCTCCACT 660

Db 595 TGGAGCTGTGGAAGCGTAGGTATCTCAGTAGGTGCGCAAGCCATCTGAGTCTGCTGCT 654

Qy 661 ACCTCTTCAGTCTTCAGGACACTTACAGAGCTGGGGTGGCTTCAGGACAAAGTAAT 720

Db 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

Qy 721 CCGTGATTTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAAGTCTCTGAAAGAAAGACGAGC 780

Db 715 TCTGATTCGACAAAGTTCTGCTATCTTCAATTCAGAGACAGAGAGAGAGAGTAGT 774

Qy 781 ATCTGTGTCTTAAAGGACTCAATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 840

Db 775 CTCAATGTTTCTTCAAGAACCAAGATGATGCAATACATATGCTTCCAAAATGGGTTC 834

Qy 841 TTTCTGGGATTCGAAAGTGTGAGCGCTTCGCCAAAGGAGTAGCAGAGCTTCTCAGAGGC 900

Db 835 TTTCTCCCAATCAGATCTCTGTAGTCTTTCACCAAGGGAACATGTTGAATCTGCTTGAAGCC 894

Qy 901 AGGAAGCTAGCAGGTCACTGCGCACTCTCTGAGCGCTTTTGCATTTTCTGGGCTCCA 960

Db 895 AGGAGATTACCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTGGGCTCCA 954  
 QY 961 TACTGCTGTTCACATGTCCTTTCACTTACCCAGACGGAGCCCAATCGGTG 1020  
 Db 955 TATTCTCTGTTCACATGTCCTTTCACTTACCCAGACGGAGCTCTAATACGATT 1014  
 QY 1021 TGGTACAGCATTCCTTCGGCTGCAATGCTCAATTCGTTTGTATTCCTTTCGTAC 1080  
 Db 1015 TGGTATAGATTGCAATTTGGCTTCAGTGGTCAATTCCTTTCGATCCTCTTTGTAT 1074  
 QY 1081 CCTTTGTGCACAGCGCTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140  
 Db 1075 CCATTGTGTGCACAGCGCTTTCAAAGGCTTTCTGAAATATTTGTATATAAAGCAA 1134  
 QY 1141 CCAGCGCTGCACAGAAC---CAGTCAGTATCTTCITGA 1176  
 Db 1135 CCTCTACCATCAACAACAGTCGGTCAGTATCTTCTTAA 1173

## RESULT 7

AAH24007  
 ID AAH24007 standard; cDNA; 1173 BP.

XX  
 AC AAH24007;

XX  
 DT 10-AUG-2001 (first entry)

XX  
 DE Human G protein-coupled receptor AXOR35 cDNA.

XX AXOR35; human; G protein-coupled receptor; 7TM receptor;  
 KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;  
 KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;  
 KW bulimia; osteoporosis; asthma; allergy; urinary retention;  
 KW acute heart failure; hypotension; hypertension; angina pectoris;  
 KW myocardial infarction; stroke; ulcer; migraine; vomiting;  
 KW psychotic disorder; neurological disorder; anxiety; schizophrenia;  
 KW manic depression; bipolar disorder; depression; delirium; dementia;  
 KW severe mental retardation; dyskinesia; Parkinson's disease;  
 KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;  
 KW macrophage; eosinophil; neutrophil; function modulation;  
 KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;  
 KW drug screening; signal transduction; transgenic animal; drug discovery;  
 SS.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1173

FT /\*tag= a

FT /product= "Human AXOR35"

FT /note= "G protein-coupled receptor"

XX WO200133221-A1.

PN 10-MAY-2001.

XX 26-OCT-2000; 2000WO-US029461.

XX 02-NOV-1999; 99US-00431898.

PR 03-FEB-2000; 2000US-00497790.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;

PI Michalovich D, Morrow DM, Zhu Y;

XX WFI; 2001-316464/33.

DR P-PSDB; AAB73622.

XX Novel G-protein coupled receptor polypeptide and polynucleotide for  
 PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological  
 PT disorders and for identifying modulators useful for treating asthma.

XX  
 PS  
 XX  
 CC The invention relates to the human G protein-coupled receptor AXOR35  
 CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments  
 CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative  
 CC transmembrane domains and is involved in signal transduction. AXOR35 has  
 CC homology and structural similarity with G protein-coupled receptors such  
 CC as the human histamine H3 receptor. The invention also relates to  
 CC expression vectors and host cells comprising AXOR35 DNA, to recombinant  
 CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins  
 CC and nucleotides may be used to treat a wide variety of disorders  
 CC including bacterial, fungal, protozoal and viral infections, particularly  
 CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;  
 CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;  
 CC urinary retention; acute heart failure; hypotension; hypertension; angina  
 CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;  
 CC psychotic and neurological disorders such as anxiety, schizophrenia,  
 CC manic depression, depression, delirium, dementia, and severe mental  
 CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's  
 CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and  
 CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and  
 CC antibodies may be used in screening compounds for their ability to  
 CC modulate AXOR35 activity or expression. Such AXOR35 modulators are  
 CC particularly useful for treating asthma, and inhibiting or promoting the  
 CC function of lymphocytes, macrophages, eosinophils or neutrophils in  
 CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also  
 CC useful for diagnosing or determining susceptibility of an individual to a  
 CC disease via the detection of abnormal levels of protein or mRNA, or via  
 CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
 CC also useful for inducing an immunological response in a mammal against  
 CC the above diseases, and for antibody production. AXOR35 nucleotides are  
 CC also useful as diagnostic reagents, in chromosome localisation and tissue  
 CC expression studies, and for producing transgenic animals useful in drug  
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
 CC protein or fragments thereof, and are also useful for treating conditions  
 CC associated with the expression of the AXOR35 protein. The present  
 CC sequence represents cDNA encoding human AXOR35  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 5; Length 1173;

Best Local Similarity 75.1%; Pred. No. 4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGAGTCTAACAGTACTGGCACTCTGCCACCAGCTGCTCAGGTCCCTTGGCAATTT 60  
 Db 1 ATGCCAGATATAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60  
 QY 61 TTAATGTCCTTCATTTCGCTTTGCTATAATGCTAGGCAATGCTGGTGCATCTTAGCCCTTT 120  
 Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATATGCTAGGAATGCTTTGGTCATTTAGCTTTT 120  
 QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT 180  
 Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACCTTGGCCATCTCT 180  
 QY 181 GACTTCCTCGTGGGTTTGATTTCATTCCTCTGTATACCTCCTCAGCTGTTGTTAACTGG 240  
 Db 181 GACTTCCTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCCTCACACGCTGTTTCAATGG 240  
 QY 241 AATTTTGGAAATGGAATCTGCATGTTTGGCTCATTTACTACTACTATCTTTTGTGCACCGCA 300  
 Db 241 GATTTTGGAAAGGAATCTGTGTAATTTTGGCTCACTACTACTACTATCTGTTATGTACAGCA 300  
 QY 301 TCTGTCTACAAATATTTGTCCTCATTAGCTACGATCGATACCAAGTCAGTTTCAAAATGCTGTG 360  
 Db 301 TCTGTATATAACATTTGTCCTCATCAGCTATGATCGATACCTGTTCAGTCTCAAAATGCTGTG 360  
 QY 361 TCTTATAGGCTCAACACACATCGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420  
 Db 361 TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTTTACTCTCTGATGGTGGCGCTTTGG 420

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QY 421 ATACTGGCTTCTTGGTAATGGCCGATGATCTGCTTTCAGATTTCTTGGAGAACAGC 480
Db 421 GTGTGGCTTCTTGGTAATGGCCGATGATCTGCTTTCAGATTTCTTGGAGAACAGC 476
QY 481 ACAGAACACAAAGGACTGTGAGCCTGGCTTTGTACAGAGTGGTACATCTCCACATTAACA 540
Db 477 --TGAAGGTAGTGAATGTAACCTGGATTTTTCGGAATGGTACATCTCCACATTAACA 534
QY 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTTAC 600
Db 535 TCATTTCTTGAATTCCTGATCCAGTCACTCTAGTCGCTTATTTCAACATGAATATTTAT 594
QY 601 TGGAGCTGTGGAGGCTAGGGCTCTCAGTAGTGGCTTAGCCATGCTGGATTTCTCACT 660
Db 595 TGGAGCTGTGGAGGCTAGATCATCTCAGTAGTGGCTTAGCCATGCTGGAGCTGAGCTGCT 654
QY 661 ACCTCTTCCAGTCTTTCAGGACATTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CTGGATTTGAAGAAATCAGTGTGATCTGTCATCTCAGAAAGTCTCTGAGAAAGAGAGC 780
Db 715 TCTGCAATCGACAGAAAGTCTGTCATCTTCAATTCAGAGAGACAGAGAGAGAGAGTAGT 774
QY 781 ATCTGTGTCTTAAAGACTCATATGAACAGCAGATATCACTGCTTCAAGTGGGTTC 840
Db 775 CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATTCCTTCCAAATGGGTTC 834
QY 841 TTCTGCGATCGAAAGTGCAGGCTTTCGCCAAAGGAGTACGACAGCTTCTCAGAGGC 900
Db 835 TTCTCCATCAGATCTGTAGTCTTTCACCAAGGAGACATGTTGACTGCTTAGGCC 894
QY 901 AGGAAGTACGAGGCTCAGTGGCCATCTTCTCAGCGCTTTTCCCATTTGCTGGGTCCA 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTGTGCTGGGTCCA 954
QY 961 TACTGTCTGTTCATTTGCTTCTTCACTTCACTTCCAGAGAGGAGCCCAATCGGTG 1020
Db 955 TATCTCTGTTCATTTGCTTCTTCACTTCACTTCCAGAGAGGCTTCAAAATCAGTT 1014
QY 1021 TGGTACAGATTCCTTCTGCTGCAATGGTTCATTTGCTTCAATCTTCTTCTGTAC 1080
Db 1015 TGGTATGAAATTCATTTTGGCTTCAGTGGTTCATTTCTTCTCAATCTTCTTGTAT 1074
QY 1081 CTTTGTGTACAGGCTTTCAGAGGCTTTCGAAAGATCTTGTGAGACAAAGCAA 1140
Db 1075 CCATTTGTTCACAGGCTTTCAGAGGCTTTCGAAAGGCTTTCGAAATATTTGTATATAAAGCAA 1134
QY 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 8
ID ABZ80663 standard; cDNA; 1173 BP.
XX
AC ABZ80663;
XX
DT 13-JUN-2003 (first entry)
XX
DE Human histamine receptor coding sequence.
XX
KW human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;
KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
KW anti-migraine; cardiant; anti-rheumatic; anti-arthritis; antipsoriatic;
KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
KW psoriasis; receptor.
XX
OS Homo sapiens.
XX
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PH Key Location/Qualifiers
FT CDS 1..1173
FT /tag= a
FT /product= "Histamine receptor"
XX
XX US6204017-B1.
XX
XX 20-MAR-2001.
XX
XX 07-OCT-1999; 99US-00414010.
XX
XX 07-OCT-1999; 99US-00414010.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Behan JX, Hedrick JA, Laz TM, Monsma FU, Morse KL, Umland SP;
XX Wang S;
XX
XX WPI: 2002-442063/47.
XX P-PSDB; ABO98629.
XX
XX New nucleic acid encoding antigenic part of human histamine receptor,
XX useful for preparing antibodies, e.g. for treating-histamine related
XX disorders.
XX
XX Example 1; Col 27-28; 19pp; English.
XX
XX This sequence represents the open reading frame for a human histamine
XX receptor (HR) designated SP9144. The sequence was isolated by searching
XX databases with the sequence of known G-coupled protein receptor (GPCR).
XX The gene is used for recombinant production of HR and for preparing
XX antibodies (Ab). These Ab are used to purify HR by immunoaffinity
XX chromatography, in immunoassay of histamine receptor, to identify cDNA
XX clones that express the receptor, as antagonist to block binding of
XX histamine (for treating any histamine-associated disorder) and to
XX generate anti-idiotypic antibodies. Agonists and antagonists of the HR
XX protein can be used in the treatment of e.g. inflammation, asthma,
XX allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
XX chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
XX sclerosis, inflammatory bowel disease and psoriasis
XX
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCATTT 60
Db 1 ATGCCAGATCTAATAGCAATCAATTTATCTAAGCACTCGTGTACTTTAGCATTT 60
QY 61 TTAATGTCTTCAPTTTCCTTTTGTCTATAATAGTGGCAATGCTGTGGTCATCTTAGCCTTT 120
Db 61 TTTATGTCTTAGTAGCTTTTGTCTATAATAGTGGCAATGCTTTGGTCATTTTAGCTTTT 120
QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGGTGGACAAAAACCTTAGACATCGAAGTAGTATTTTTTCTTAATTTGGCCATCTCT 180
QY 181 GACTTCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTCACGCTGTGTTTAACGTG 240
Db 181 GACTTCTTTGGGGTGTGATCTCCATTTCTTTGTATACCTCCACAGCTGTTCGAAATG 240
QY 241 AATTTTGGAAAGTGAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCACGCA 300
Db 241 GATTTTGGAAAGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATATGTACAGCA 300
QY 301 TCTGTCTACAATATTCCTCTCATTTAGTACGATACGATACAGTCAGTTTCAAAATGCTGTG 360
Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATACGATACCTGTCAAGTCTCAAAATGCTGTG 360
QY 361 TCTTATAGGCTCAACACACTGGCATCAAGATTTGTTCTCAAAATGGTGGCTGTTTGG 420
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Db      361  TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCGCTTTGG 420
Qy      421  ATACTGGCTTTCTTGGTAAATGGCCCAATGATTCCTGGCTTCAGATTCTTGGAGAACAGC 480
Db      421  GTGCTGGCTTCTTGTAGTGAATGGCCCAATGATTCAGTTTTCAGAGTCTTGGAAAGGA---- 476
Qy      481  ACGAACAACAAGGACTGTGAGCCTGGCTTGTCTTACAGAGTGGTACATCCTCACCAATTACA 540
Db      477  --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCCTTGGCCATCACA 534
Qy      541  ATGCTCTTGAATTCCTGCTCTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTC 600
Db      535  TCATTCTTGAATTCGTGATCCCAATCTTAGTGGCTTATTTCAATGAATATTTAT 594
Qy      601  TGAAGCTGTGGAAGCCTAGGGCTCTCAGTAGGTGCCCCTAGCCATGCTGGAATTCCTCACT 660
Db      595  TGAAGCCTGTGGAAGCCTGATCATCTCAGTAGGTGCCAAAGCCATCCTGGACTGACTGCT 654
Qy      661  ACCTCTCCAGTGCTTCAGACACATTCACAGAGCTGGGTGGCTTCGAGGACAAAGTAAT 720
Db      655  GTCTCTTCCAACTCTGTGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy      721  CCTGGATTGAAGGAATCAGCTGCTGCTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780
Db      715  TCTGCATCGACAGAGTCTCTGATCCTTTCATTCAGAGACAGAGGAGAGAGTAGT 774
Qy      781  ATCTGTGTCTTAAAGATTCATGATCAAGACAGAGTATCACTGCTTCAAGTGGGTTC 840
Db      775  CTCATGTTTCTTCAAGAACCAAGATGAATAGCAATACAATGCTTCCAAATGGGTTC 834
Qy      841  TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAGGAGTACCGAGAGTCTTCAGAGGC 900
Db      835  TTCTCCCAATCAGATCTGTAGTCTTTCACCAAGGGAACATGTTGAATGCTTAGAGCC 894
Qy      901  AGGAAGCTAGCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db      895  AGGAGATTACCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGCTCCA 954
Qy      961  TACTGTCTGTCAAAATGTCCTTTCAACTTACCCAGAACCGGAACGCCCAATCGGTG 1020
Db      955  TATTTCTGTGTCAAAATGTCCTTTCAATTTATTTCTCAGCAACAGGTCCTTAAATCAGTT 1014
Qy      1021  TGTACAGCATTCCTCTCGCTGCAATGTTCAATTCGTTGTTGTTAATCCCTTCTGTAC 1080
Db      1015  TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTTCCCTTTGTCATCTCTTTGTAT 1074
Qy      1081  CCTTTGTGTACAGCGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGCACAAAGCAA 1140
Db      1075  CCATTGTGTACAGCGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAA 1134
Qy      1141  CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTTGA 1176
Db      1135  CCTTACCATCACAAACAGTCGGTCAGTATCTTCTTAA 1173
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## RESULT 11

ACA93262  
ID ACA93262 standard; cdna; 1173 BP.

XX ACA93262;

XX 16-JUL-2003 (first entry)

XX Human cdna encoding GPCR hrup7.

XX Human; ss: gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
hARE-5; hrup3; hrup5; hrup6; hrup7; hGPCR27; hARE-1; hARE-2; hrup1; hG2A;  
hCHN3; hCHN4; hCHN6; hCHN9; hCHN10; hruf4; signalling cascade.

XX Homo sapiens.

XX US2003017528-A1.

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XX 23-JAN-2003.
XX 06-JUN-2001; 2001US-00875076.
XX 20-NOV-1998; 98US-0109213P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123949P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136567P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 29-JUN-1999; 99US-0141448P.
XX 28-SEP-1999; 99US-0156333P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156634P.
XX 12-OCT-1999; 99US-00417044.
XX (CHEN/) CHEN R.
XX (DANG/) DANG H T.
XX (LIAW/) LIAW C W.
XX (LINI/) LIN I.
XX Chen R, Dang HT, Liaw CW, Lin I;
XX WPI; 2003-428952/40.
XX P-PSDB; ABU92265.
XX Novel endogenous, orphan, human G protein-coupled receptors useful for
XX identification of modulators of the receptor and as research tools for
XX understanding the role of the receptor in human body.
XX Claim 25; Page 22; 54pp; English.
XX The invention relates to a human G protein-coupled receptor (GPCR)
XX appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named
XX hARE-3, hARE-4, hARE-5, hrup3, hrup5, hrup6, hrup7, hGPCR27, hARE-1, hARE
XX -2, hrup1, hG2A, hCHN3, hCHN4, hCHN6, hCHN9, hCHN10 and hruf4.
XX Also included are a plasmid comprising a vector and one of the cDNAs
XX above and a host cell comprising the plasmid. The GPCRs are useful for
XX the direct identification of candidate compounds as inverse agonists,
XX agonists or partial agonists. In vitro and in vivo systems incorporating
XX GPCRs is useful for elucidating and understanding the roles these
XX receptors play in the human condition, both normal and diseased, as well
XX as understanding the role of constitutive activation as it applies to
XX understanding the signalling cascade. The cDNAs are useful for making a
XX probe for dot-blot analysis against tissue mRNA and/or RT-PCR
XX identification of the expression of the receptor in tissue samples. The
XX present sequence is a cdna encoding a GPCR of the invention
XX
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
```

Query Match 58.4%; Score 686.6; DB 8; Length 1173;

Best Local Similarity 75.1%; Pred. No. 4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATTT 60

Db 1 ATGCCAGATCTAATAGCACAAATTAATATCACTAAGCACTCGTGTACTTTAGCAATTT 60

Qy 61 TTAATGTCCTTATTTGCTTTGCTATTAATGTTAGGCAATGCTGTGGTCATCTTAGCCTTT 120

Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTTAGCTTTT 120

Qy 121 GTGGTGACAGAACCTTAGACATCGAGTAATATTTTCTTAATTTTGGCTATTTCT 180

Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180

Qy 181 GACTTCCTCGTGGGTTTGTATTTCCATTTCCCTCTGTACATCCCTCACGTGTTGTTAACTGG 240

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Db 181 GACTTCTTTGGTGGTGAATCTCATCTCTTTTGATACCTCTCACACCTCTTCCGAATGG 240
Qy 241 AATTTTGGAGTGGAACTGCAATCTGATGTTTGGCTCAATTAAGTACTGATCTTTTGTGCACGCA 300
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
Qy 301 TCTGTCTACATATATGCTCTCAATAGCTACGATACGATACGATGATGATTTCAAAATGCTGTG 360
Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATGATACCTGTGCTCAATGCTGTG 360
Qy 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGCTGCTGTTTGG 420
Db 361 TCTTATAGAACTCAACATACATCTGGGGCTTGAAGATTTGATCTGATGCTGGCCGCTTGG 420
Qy 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480
Db 421 GTGCTGGCTTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGGGAAGA--- 476
Qy 481 ACGAACACAAAGGACTGTGAGCCCTGGCTTTGTTTACAGAGTGGTACATCTCACCATTAACA 540
Db 477 --TGAAGCTAGTGAATGTGAACCTGGATTTTTCGGAAATGGTACATCTTGGCCATCACA 534
Qy 541 ATGCTCTTGGAAATTCCTGCTTCCTGTGATCTCTCTGCTGCTTATTTCAATGTACAGATTAC 600
Db 535 TCATTTCTTGGAAATTCGATCCAGTCCATCTAGTCGCTTATTTCAACATGAATATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 660
Db 595 TGGAGCCTGTGGAAGCGTAGTATCTCAGTAGGTGCCAAGCCATCTGACTGACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTTCAAGACACTTACACAGAGCTGGGGTGGCTTCGAGACAAAGTAAT 720
Db 655 GTCTCTTCCAAACATCTGTGGACACTCACTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTGAAGGAATCAGCTGCTGCTGCTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAAGTTCCTGTCATCTTCAATTCAGAGACAGAGGAGAAAGTAGT 774
Qy 781 ATCTGTGTCTTAAAGACTCAATGAAACAGAGTATCACTGCTTCAAAAGTGGTTC 840
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATGAATCAATTTGTTCCAAAATGGGTTC 834
Qy 841 TTCTGGCGATCGGAAATGACAGCGCTTCGCCAAGGAGTACGAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTCTGATGCTTTCACCAAAGGGAACATGTTGAACCTGTAGAGCC 894
Qy 901 AGNAGCTAGCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy 961 TACTGTCTGTTCAAAATTTGCTTCAACTTTACCCAGAACGGAAACGCCCAAAATCGGTG 1020
Db 955 TATTCCTGTTCAAAATTTGCTTCAATTTATTTATTCCTCAGCAACAGGCTCTTAATCAATT 1014
Qy 1021 TGGTACAGCATTTGCTTCTGGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080
Db 1015 TGGTATAGAAATGCAATTTGGCTTCACTGAGTTCATTTCCCTTTGTCAATCCCTTTTGTAT 1074
Qy 1081 CTTTGTGTACAGGCGTTTCCAGAAGCTTTCTGGAAGATACATTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGTACAGGCGTTTCCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAA 1134
Qy 1141 CCAGCGCTGTACAGAAC---CAGTCAAGTATCTCTGA 1176
Db 1135 CCTTACCATCAACAACAGAGTCGGTCTAGTATCTTCTTAA 1173
```

RESULT 12

ADG98759

ID ADG98759 standard; cDNA; 1173 BP.

XX

AC ADG98759;

```
XX 11-MAR-2004 (first entry)
XX Human orphan GPCR cDNA, RUP7.
XX Human; G protein-coupled receptor; GPCR; research tool; gene; ee.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..1173
XX /*tag= a
XX /product= "Human GPCR protein"
XX US2003148450-A1.
XX 07-AUG-2003.
XX 17-OCT-2002; 2002US-00272983.
XX 20-NOV-1998; 98US-0109213P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123946P.
XX 28-MAY-1999; 99US-0136433P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136439P.
XX 28-MAY-1999; 99US-0136567P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 29-JUN-1999; 99US-0141448P.
XX 28-SEP-1999; 99US-0156333P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156634P.
XX 12-OCT-1999; 99US-00417044.
XX (CHEN/) CHEN R.
XX (DANG/) DANG H T.
XX (LIAW/) LIAW C W.
XX (LINI/) LIN I.
XX Chen R, Dang HT, Liaw CW, Lin I;
XX WPI; 2003-897571/82.
XX P-PSDB; ADG98760.
XX New cDNA encoding a human G protein coupled receptor, useful for making a
XX probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR
XX identification of the expression of the receptor in tissue samples.
XX Claim 25; SEQ ID NO 13; 52pp; English.
XX The present invention provides novel human G protein-coupled receptor
XX (GPCR) proteins and their encoding nucleic acids. The invention is useful
XX for making a probe for dot-blot analysis and for RT-PCR identification of
XX the expression of the receptor in tissue samples. The invention is also
XX useful for identifying candidate compounds as inverse agonists, agonists
XX or partial agonists and as research tools in determining the location of
XX the receptors within the body. The present sequence is human orphan G
XX protein-coupled receptor cDNA.
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX Query Match 58.4%; Score 686.6; DB 10; Length 1173;
XX Best Local Similarity 75.1%; Pred. No. 4e-204;
XX Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
Qy 1 ATGTGGGAGTCTAACAGTACTGTCACAGCTGCTCAGGTCCCTTGGCATT 60
Db 1 ATGCCAGATACTAATAGCAACAATTTATCACTAAGCACTGCTGTACTTTAGCATTT 60
Qy 61 TTAATGTCTTTCATTGCTTTTGTCTTATTAATGTTAGGCAATGCTGTGTCATCTTAGCCCTTT 120
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CC vaccines, or for treating infections (bacterial, fungal, protozoan or  
 CC viral infections), transplant rejection, gastrointestinal disorders (such  
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),  
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic  
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,  
 CC psoriasis), urological diseases (such as urinary retention),  
 CC cardiovascular diseases (such as myocardial infarction), hypotension,  
 CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary  
 CC disease), cough, renal diseases (such as renal ischaemia);  
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such  
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft  
 CC versus host disease and osteoporosis. The present sequence is the cDNA  
 CC encoding AXOR35

XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 10; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 4e-204;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCACACAGCTGCTCAGGTCCCTTGGCAATTT 60  
 DB 1 ATGCCAGATCTAATAGCACAAATCAATTTATCACTAAGCACTGCTTACTTTAGCAATTT 60  
 QY 61 TTAATGTCCTTCAATTTGGCTTTGCTATTAATGGTAGGCAATGCTGGTGCATCTTAGCCCTTT 120  
 DB 61 TTTATGTCCTTCAATTTGGCTTTGCTATTAATGGTAGGCAATGCTTTGGTGCATCTTAGCTTTT 120  
 QY 121 GTGGTGACAGAAACCTTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
 DB 121 GTGGTGACAGAAACCTTTAGACATCGAAGTAGTATTTTCTTAATTTGGCTATTTCT 180  
 QY 181 GACTTCTCGTGGGTTTGAATTTTCATTCCTCTGTACATCCCTCACGCTGTTGTTAACTGG 240  
 DB 181 GACTTCTTGTGGTGTGATCTCAATTCCTTTGTACATCCCTCACGCTGTTGCGAATGG 240  
 QY 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300  
 DB 241 GAATTTTGGAAAGAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300  
 QY 301 TCTGTCTACAAATATGTCCTCAATTAGCTACGATCGATCAGTACAGTTCCTCAATGCTGTG 360  
 DB 301 TCTGTATATAACATATGTCCTCAATTAGCTACGATCGATCAGTTCCTCAATGCTGTG 360  
 QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGGTGGCTGTTTGG 420  
 DB 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTGG 420  
 QY 421 ATACTGGCTTCTTGGTGAATGGCCGATGATTTCTGGCTTCAGATTCTTGGAAAGACAGC 480  
 DB 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGGA--- 476  
 QY 481 ACGAACACAAGACCTGTGAGCTGGCTGTTTGTACAGAGTGGTACATCCTCACCATTACA 540  
 DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGGCATACA 534  
 QY 541 ATGCTCTTGAATTCCTGCTTCTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600  
 DB 535 TCATTTCTTGAATTCGTGATCCCGATCATCTTAGTCGTTATTTCAACATGAATATTTAT 594  
 QY 601 TGGAGCTGTGGAAAGCGTAGGGCTCTCAGTAGGTGCGCTTAGCCATGCGATGCTTCTCACT 660  
 DB 595 TGGAGCTGTGGAAAGCGTAGATCATCTCAGTAGGTGCGCAAGCCATCTCGACTGACTGCT 654  
 QY 661 ACTCTTCCAGTCTTTCAGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720  
 DB 655 GTCTCTTCCAACTCTGTGGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
 QY 721 CCTGGATTGAAGAAATCAGCTGATCTCGTCACTCAGAAAGTCTCTGAAAGAAAGAGCAGC 780  
 DB 715 TCTGCATCGACAGAAAGTCTCTGCATCTCTTCAATTCAGAGAGACAGAGGAAAGAGTAGT 774

QY 781 ATCTGTGTGCTTTAAGGACTCAGATCAAGACAGCAGTATCACTGCTTCAAGTGGGTTC 840  
 DB 775 CTATGTTTTCCTTCAAGAAACCAAGATGATAGCAATCAATTTGCTTCAAAATGGGTTC 834  
 QY 841 TTCTGGCGATCGGAAAGCTGCGAGCGCTTCGCCAAAGGGAGTACGACAGAGCTTCTCAGAGGC 900  
 DB 835 TTCTCCCAATCAGATCTGTAGCTCTTTCACCAAGGGAACATGTTGAATGCTTTAGAGCC 894  
 QY 901 AGGAAGCTACCGAGGTCACTGGCCATCTTCTGTAGCGCTTTTGGCATTTGCTGGGCTCCA 960  
 DB 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954  
 QY 961 TACTGTCTGTTCACAAATGTCCTTCACTTACCCAGAGCGGACGCCCAAAATCGGTG 1020  
 DB 955 TATTTCTCTGTTCACAAATGTCCTTCAATTTTATTTCTCAGCAACAGGTCCTAAATCAGTT 1014  
 QY 1021 TGGTACAGCAATGCTTCTGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTGAC 1080  
 DB 1015 TGGTATAGAAATGCAATTTGGCTTTCAGTGGTTCATTTCTTGTCAATCTCTTTTGTAT 1074  
 QY 1081 CCTTTGTGTACAGGCGTTTCCAGAAAGGCTTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140  
 DB 1075 CCATTTGTGTACAGGCGTTTCCAAAGGCTTTCTTGAATAATATTTGTATATAAAAGCAA 1134  
 QY 1141 CGAGCGCTGTACAGAAC---CAGTCAGTATCTCTTGA 1176  
 DB 1135 CCTTACCATCAACACACAGTCGGTCAGTATCTCTTAA 1173

RESULT 14  
 ADJ26922  
 ID ADJ26922 standard; cDNA; 1173 BP.  
 XX AC ADJ26922;  
 XX AC (first entry)  
 DT 20-MAY-2004  
 XX Human endogenous orphan G-protein coupled receptor RUP7 cDNA.  
 DE Human; G protein-coupled receptor; GPCR; dot-blot analysis;  
 KW pharmaceutical agent; gene; ss.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 CDS 1..1173  
 FT /\*tag= a  
 FT /product= "Human endogenous orphan GPCR protein"  
 XX US2003175891-A1.  
 XX 18-SEP-2003.  
 XX 21-MAR-2003; 2003US-00393807.  
 PF 20-NOV-1998; 98US-0109213P.  
 XX 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 28-JUN-1999; 99US-0141448P.  
 PR 28-SEP-1999; 99US-0156333P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.

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PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00417044.
PR 17-OCT-2002; 2002US-00272983.
XX
CHEN R.
PA (DANG/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAN/) LIAN C W.
PA (LINI/) LIN I.
XX
Chen R, Dang HT, Liaw CW, Lin I;
XX
WPI: 2003-898539/82.
DR P-PSDB; ADJ26923.
XX
New human G protein-coupled receptor and its coding cDNA, useful for
PT disease or disorder identification and/or selection, for screening of
PT candidate compounds useful as pharmaceutical agents, and in research
PT applications.
XX
Claim 25; SEQ ID NO 13; 53pp; English.
XX
The present invention relates to human endogenous orphan G protein-
CC coupled receptor (GPCR) proteins and polynucleotides encoding such
CC proteins. The cDNA sequence of the human G protein-coupled receptor
CC (GPCR) is useful in making a probe for dot-blot analysis against tissue-
CC mRNA and/or for RT-PCR identification of the expression of the receptor
CC in tissue samples. GPCR sequences of the invention may be used in
CC disease/disorder identification and/or selection, in screening of
CC candidate compounds for use as pharmaceutical agents and in research
CC settings. The present sequence is human endogenous orphan GPCR cDNA.
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
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Query Match 58.4%; Score 686.6; DB 11; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
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QY 1 ATGTCGAGTCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGTCCCTGGCATTTT 60
DB 1 ATGCCAGATCTAATAGCACAAATCAATTATCATCAAGCACTCGTGTACTTTAGCATTT 60
QY 61 TTAATGCTTTCATTGCTTTCATTAATGCTAGGCAATGCTGGTCACTTTCAGCCTTT 120
DB 61 TTAATGCTTTCATTGCTTTCATTAATGCTAGGCAATGCTGGTCACTTTCAGCCTTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTAATTTCT 180
DB 121 GTGGTGACAGAAACCTTAGACATCGAAGTAGTTAATTTTCTTAATTTGGCCATCTCT 180
QY 181 GACTTCCTCGTGGTTTGATTTTCATTCCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240
DB 181 GACTTCCTTGTGGTGTGATCTCCTCAATTCCTTGTACATCCCTCAGCTGTTGTTAACTGG 240
QY 241 AATTTTGGAGTGAATCTGCATGCTTTGGTCAATTAATTAATTAATTTGGTCAACCGCA 300
DB 241 GAITTTTGGAAAGGAATCTGTGTAATTTGGTCAATTAATTAATTTGGTCAACCGCA 300
QY 301 TCTGCTACAAATATTTGCTCATTAGTACGATCGATACCAAGTCAAGTTTCAAAATGCTGTG 360
DB 301 TCTGTATATAACATTGTCCTCATCAGCTATGATGATACCTGTGTCAGTCTCAAAATGCTGTG 360
QY 361 TCTTATAGGGCTCAACACATGGCATCATGAAGATTGTTGCTCAAAATGTTGGCTGTTTGG 420
DB 361 TCTTATAGAACTCAACATCTAGTGGGCTTCTGAAGATTGTTTACTCTGATGGTGGCGGTTTGG 420
QY 421 ATACTGCTTCTTTGGTGAATGSCCGCATGATTTCTGCTTCAGATTCTTGAAGAACAGC 480
DB 421 GTGCTGGCTTCTTAGTGAATGGCCAAATGAATTTCTAGTTTCAGAGTCTTGAAGGA --- 476
QY 481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACA 540
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DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTCGGAATGGTACATCTTGGCATCACA 534
QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGTCATCTCTGTCATCTTATTTCAATGTACAGATTAC 600
DB 535 TCATTTCTTGAATTCGTGATCCAGTCATCTTAGTGCCTTATTTTCAATGAATATTTAT 594
QY 601 TGGAGCTCTGTGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTTCCACT 660
DB 595 TGGAGCTCTGTGAAGCGTAGTCATCTCAGTAGGTGCCAAAGCCATCTGAGCTGACTGCT 654
QY 661 ACCTCTTCAGTCTTCAGGACACTTACAGAGCTGGGGTGGCTTCAGGACAGAGTAAT 720
DB 655 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714
QY 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAAGTCTCTCGAAGAAAGAGCAGC 780
DB 715 TCTGCAATCGAAGATTCTCTGCATCTTTCATTCAGAGACAGAGAGAGAGTAGT 774
QY 781 ATCTCTGTGTCTTAAAGGACTCAGTGAACAGCAGATATCACTGCTTCAAAAGTGGGTTC 840
DB 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATAGTCTTCCAAAATGGGTTC 834
QY 841 TTTCTGGGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGC 900
DB 835 TTTCTCCCAATCAGATTCTGTAGCTCTTCAACAAAGGGAAACATGTTGAATCTGTAGAGC 894
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCATTTTCTGCTGGGCTCCA 960
DB 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTTAGGGGTTTTTGTCTGTTGCTGGGCTCCA 954
QY 961 TACTGTCTGTTTCAAAATGTCTTCAACTTATCCAGAAACCGAAACCGCCCAATCGGTG 1020
DB 955 TATTCTCTGTTCAAAATGTCTTCACTTATTTTCTCAGCAACAGGTCTCTAAATCAGTT 1014
QY 1021 TGTGACAGCATTCGCTTCTGGCTGCAATGGTTCAATTCGTTTGTAACTCTTCTGCTAC 1080
DB 1015 TGTGATAGAAATTCGATTTTGGCTTTCAGTGGTTCAAATTCCTTGTCAATCTCTTGTGAT 1074
QY 1081 CCTTTGTGTCACAGGCTTTCCAGAAAGGCTTTCTGGAAGATACCTTTGTGACAAAGCAA 1140
DB 1075 CCATTGTTGTCACAAAGGCTTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAGCAA 1134
QY 1141 CCAGCGCTGTGCACAGAAC---CAGTCAGTATCTTCTTGA 1176
DB 1135 CCTCTACCATCACACACAGCTGCTGATCTCTTTAA 1173
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```
RESULT 15
ADG86374
ID ADG86374 standard; cDNA; 1173 BP.
XX
AC ADG86374;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human endogenous orphan GPCR hrup7 cDNA.
XX
KW Human; ss; gene; endogenous orphan GPCR; G protein-coupled receptor;
KW transmembrane domain 6.
OS Homo sapiens.
XX
PN US2003229216-A1.
XX
PD 11-DEC-2003.
XX
PF 16-APR-2003; 2003US-00417820.
XX
PR 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
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PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123944P.  
 PR 12-MAR-1999; 99US-0123945P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123948P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 12-MAR-1999; 99US-0123951P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 28-JUN-1999; 99US-0141448P.  
 PR 27-AUG-1999; 99US-0151114P.  
 PR 03-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 XX  
 PA (CHEN/) CHEN R.  
 PA (LIAN/) LIAN C W.  
 PA (LOWI/) LOWITZ K.  
 PA (CHAL/) CHALMERS D T.  
 PA (BEHA/) BEHAN D P.  
 XX  
 PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;  
 XX  
 DR WPI; 2004-052038/05.  
 DR P-PSDB; ADG86375.  
 XX  
 PT New cDNA encoding a non-endogenous, constitutively activated version of a  
 PT human G protein-coupled receptor, useful for identifying receptor,  
 PT inverse or partial agonists having potential applicability as therapeutic  
 PT agents.  
 XX  
 PS Example 1; SEQ ID NO 13; 110pp; English.  
 XX  
 CC The invention relates to a cDNA encoding a non-endogenous, constitutively  
 CC activated version of a human G protein-coupled receptor comprising hARE-  
 CC 3 (F313K), hARE-4 (V233K), hARE-5 (A240K), hGPCR14 (L257K), hGPCR27 (C283K),  
 CC hARE-1 (E323K), hARE-2 (G285K), hPR1 (L2319K), hG2A (K232A), hRUP3 (L224K),  
 CC hRUP5 (A236K), hRUP6 (N267K), hRUP7 (A302K), hCHN4 (V236K), hMC4 (V244K),  
 CC hCHN3 (S284K), hCHN6 (L352K), hCHN8 (N235K) or hH9 (F236K). Also included are  
 CC a non-endogenous version of a human G protein-coupled receptor encoded by  
 CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell  
 CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively  
 CC activated version of a human G protein-coupled ARI receptor comprising  
 CC the angiotensin II type 1 receptor hAT1 (F239K), hAT1 (N111A),  
 CC hAT1 (AT24551C3, a domain swap mutant) or hAT1 (A243+). The mutation is of  
 CC an amino acid 16 residues from the proline in transmembrane domain 6 and  
 CC is usually to a lysine. The cDNA is useful for identifying candidate  
 CC compounds as receptor agonists, inverse agonists or partial agonists  
 CC having potential applicability as therapeutic agents. The present  
 CC sequence is a cDNA (or fragment) for a wild-type human GPCR.  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 58.4%; Score 686.6; DB 12; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 4e-204;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
 1 ATGTCGGAGCTACAGTACTGGCATCTTGGCCACGCTGCTCAGTCCCGCTTGGCATTT 60  
 1 ATGCCAGATACTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60

QY 61 TTAATGCTTTCATTTGCTTTGCTTATTAATGGTAGGCAATGCTGGTCACTCTTAGCCCTTT 120  
 DB 61 TTTATGTCCTTAGTAGCTTTTGGCTATTAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120  
 QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180  
 DB 121 GTGGTGACAGAAACCTTAGACATCGAAGTAGTATTTTTTCTTAATTTGGCTATTTCT 180  
 QY 181 GACTTCTCTGFGGGTTTGAATTCCTCTGTACATCCCTCAGTGTGTTGTTAACTGG 240  
 DB 181 GACTTCTTTTGGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGTGTGTTGTTAACTGG 240  
 QY 241 AATTTTGGAGTGGAAATCTGCATGTTTTGGTCTCAATTAAGTACTATCTTTTGGACCCCA 300  
 DB 241 GATTTTGGAGAGGAAATCTGTGATTTTTGGTCTCAATTAAGTACTATCTTTTGGACCA 300  
 QY 301 TCTGCTACAAATATTTGCTCATTAGCTACGATCAGATCAGTCTCAGTCTTCAATGCTGTG 360  
 DB 301 TCTGTATATACATTTGCTCCTCATCAGCTATGATCAGTCTCAGTCTCAGTCTCAATGCTGTG 360  
 QY 361 TCTTATAGGGCTCAACAACATCTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTTTGG 420  
 DB 361 TCTTATAGAACTCAACATCTAGGGTCTTGAAGATTGTTACTCTGATGGTGGCGGTTGG 420  
 QY 421 ATACTGGCTTTCTGGTAAATGGCCCGATGATTTCTGCTTCAGATTTCTTGAAGAACAGC 480  
 DB 421 GTGCTGGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGAAGGA 476  
 QY 481 ACGAACACAAAGGACTCTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA 540  
 DB 477 --TGAAGTAGTGAATGTGAACCTGGATTGTTTTCGGAATGGTACATCCTTGGCCATACA 534  
 QY 541 ATGCTCTTGGAAATTCCTGCTTCATCTCTGCTGCTTATTTCAATGTACAGATTTCAC 600  
 DB 535 TCATTCTTGGAAATTCGTGATCCCAAGTCACTCTTAGTCTGCTTATTTCAACATGAATTTAT 594  
 QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTTCTCCACT 660  
 DB 595 TGGAGCCTGTGGAAGCGTAGTATCTCAGTAGGTGCCCAAGCCATCTCGGAGTCACTGCT 654  
 QY 661 ACCTCTTCCAGTGTCTCAGAGACCTTACACAGAGCTGGGGTGGTTCGACGACAAAGTAAT 720  
 DB 655 GTCTCTTCCAAACATCTGTGGACACTCAATCAGAGTAGACTATCTTCAAGAGAGATCTCTT 714  
 QY 721 CCTGGATTGAAGGAATCAGCTGCACTCTGCACTCAGAAAGTCTCTCGAAAGAAAGACGACG 780  
 DB 715 TCTGCATCGACAGAAGTTCTGCACTCTTCAATTCAGAGAGACAGAGAGAGAGTAGT 774  
 QY 781 ATCTGTGTGCTTAAAGACTCAATGAAACAGAGATGATCACTGCTTCAAAAGTGGTTC 840  
 DB 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGGTTC 834  
 QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAGGGAGTACGACAGAGCTTCTCAGAGGC 900  
 DB 835 TTCTCCCAATCAGATTCGTAGCTCTTCAACAAAGGGAACATGTTGAATCTCTTAGACC 894  
 QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCATTTGCTGGGCTCCA 960  
 DB 895 AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTTTGGTGTGCTGGGCTCCA 954  
 QY 961 TACTGTCTGTACAATTTGCTTTCAATTTACCCAGAGAGCGGAAACGCCCAATTCGGTG 1020  
 DB 955 TATTCTCTGTTCAAAATTTGCTTTCAATTTATTTCTCAGCAACAGAGTCTTAAATCAGTT 1014  
 QY 1021 TGGTACAGCATTTGCTTCTGCTGCAATGTTGCTTGAATTTGTTAAATCCCTTTCTGTAC 1080  
 DB 1015 TGGTATAGAAATTCGATTTGGCTTTCAGTGGTTCATTTCTTTGCAATCTCTTTTGTAT 1074  
 QY 1081 CCTTTGTGTACAGCGCTTTCCAGAGGCTTTCTGGAAGATGATCTTTGTGTGACAAAGCAA 1140  
 DB 1075 CCATTGTGTACAGCGCTTTCAAAAGGCTTTCTTGAATATATTTGTATATAAAGCAA 1134  
 QY 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTTCTTGA 1176

Db 1135 CCTTACCAATCACACACACAGTCGGTCAGTATCTTTAA 1173

Search completed: May 22, 2006, 19:21:36  
Job time : 761 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 19:24:55 ; Search time 6433 Seconds  
(without alignments)  
10222.468 Million cell updates/sec

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Perfect score: 1176  
Sequence: 1 atctcgagctcaacagctac.....accagtcagtatcttcttga 1176

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_btc.\*  
7: gb\_est2.\*  
8: gb\_est7.\*  
9: gb\_est8.\*  
10: gb\_est9.\*  
11: gb\_gss1.\*  
12: gb\_gss2.\*  
13: gb\_gss3.\*  
14: gb\_gss4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	438.6	37.3	839	4	BX643713
2	426.4	36.3	704	5	CF147821
3	258	21.9	721	8	CO959034
4	140.8	12.0	2625	6	AK140374
5	139	11.8	791	10	DW582260
6	135.8	11.5	672	4	CB558920
7	133.8	11.4	732	5	CF147822
8	130.2	11.1	728	10	DT257276
9	129.2	11.0	558	9	DA308555
10	129.2	11.0	853	5	CD326085
11	126.8	10.8	542	10	DW576242
12	115.6	9.8	684	12	CC481311
13	114	9.7	574	9	DA306992
14	106	9.0	755	9	DA728518
15	101.2	8.6	687	10	DY313565
16	100.2	8.5	647	10	DV880423
17	99	8.4	643	1	AL848045
18	99	8.4	824	9	CX422842
19	96.2	8.2	716	8	CN423054

20	95.8	8.1	569	9	DA257272
21	95.6	8.1	499	7	BF567596
22	95	8.1	575	9	DA360011
23	88.6	7.5	1046	3	BQ950659
24	87.6	7.4	921	14	CNS03296
25	82	7.0	838	10	DV891040
26	80.6	6.9	700	8	CO138455
27	80.6	6.9	754	3	BU468854
28	80.4	6.8	505	3	BQ837058
29	80.2	6.8	258	7	AW654609
30	78.8	6.7	410	3	BQ836551
31	77.8	6.6	814	10	DT311294
32	77.6	6.6	727	8	CR366545
33	75.8	6.5	553	10	DW582261
34	75.8	6.4	523	2	BJ122942
35	75.8	6.4	565	4	CB385348
36	75.8	6.4	582	2	BJ108530
37	75.8	6.4	633	2	BJ763892
38	75.6	6.4	1136	6	BC019470
39	74.8	6.4	562	2	BJ103964
40	74.8	6.4	566	2	BJ119403
41	74.2	6.3	697	3	BU446363
42	74	6.3	781	8	CK240157
43	74	6.3	890	2	BI731453
44	74	6.3	1946	6	AK156130
45	73.4	6.2	281	7	BB592940

#### ALIGNMENTS

RESULT 1  
BX643713  
LOCUS  
DEFINITION BX643713 839 bp mRNA linear EST 04-SEP-2003  
DKFZp781C0629-5', mRNA sequence.  
ACCESSION BX643713  
VERSION BX643713.1 GI:34478046  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 839)  
AUTHORS Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
TITLE EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp781C0629) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

#### FEATURES

source  
1. 839  
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#### ORIGIN

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Best Local Similarity 75.9%; Pred. No. 3 re-118;
Matches 570; Conservative 0; Mismatches 174; Indels 7; Gaps 2;

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QY 721 CCTGGATTGAAGGAATCAGCTGTCATCTCGTC 751
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RESULT 2
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DEFINITION AGENCOURT_14740195 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971900 5', mRNA sequence.
CF147821
VERSION CF147821.1 GI:33244089
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
```

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgaps-i@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRBI02 row: b column: 07  
High quality sequence stop: 685.

FEATURES  
source

1. 704  
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/clone="IMAGE:6971900"  
/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_145"  
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varies by clone; ORFs were PCR-amplified and cloned into  
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clone represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRBI.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 36.3%; Score 426.4; DB 5; Length 704;  
Best Local Similarity 77.0%; Pred. No. 1.5e-114;  
Matches 547; Conservative 0; Mismatches 156; Indels 7; Gaps 2;  
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Db 1 GCCAGATCTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTTT 60  
QY 63 AATGCTCTTCAATTTGGCTTTCCTATATGTAGGCAATGCTGTGTCATCTTAGCTTTGT 122  
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QY 423 ACTGGCTTCTTGTAAATGSCCGATGATTTCTGGCTTCAGATTCCTTGGGAAGACAGCAC 482  
Db 421 GCTGGCTTCTTGTAGTGAATGGGCCAATGATTTAGTTTTCAGATCTTGGGAAGGA 474  
QY 483 GAACACAAAGGACTGTGAGCTTGGCTTTTGTATACAGAGTGGTACATCTCTCACCATTACAAT 542

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Db      475  TGAAGTAGTGAATGTGAACCTGATTTTTCGGAATGGTACATCTTGCCATCATC 534
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Db      535  ATTCTTGAATTCGTGATCCAGTCATCTAGTCGCTTATTTCAACATGAATATTATTG 594
Qy      603  GAGCCTGTGAAGCGTAGGCTCTCAGTAGTGGCCCTAGCAGCATCGATTCCTCATAC 662
Db      595  GAGCCTGTGAAGCGTGATCATCTCAGTAGTGGCCAAAGCCATCCTGGAGTACTGCTG 654
Qy      663  CTCTTCAGTGTCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGA 712
Db      655  CTCTTCACATC-TGTGGACACTCATTCAGAGGTAGACTATCTTTCAGGA 703

RESULT 3
LOCUS   CO959034
DEFINITION AGENCOURT 30842625 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389774 5', mRNA sequence.
ACCESSION CO959034
VERSION    CO959034.1 GI:51323616
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: gcaps-remail.nih.gov
           Tissue Procurement: Guthrie cDNA Resource Center
           cDNA Library Preparation: Guthrie cDNA Resource Center
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
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                into pCDNA3.1. For specific information on cloning sites
                (which vary by clone), please refer to the Guthrie
                website, using the Guthrie ID given in the file
                ftp://image.llnl.gov/image/rearrayed_plates/IRBF.presv.dat
                a. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.9%; Score 258; DB 8; Length 721;
Best Local Similarity 78.4%; Pred. No. 1.4e-64;
Matches 309; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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Db      22  ATGCCAGTACTAATAGCACAAATTTATCTAAGCACTCGTGTACTTTAGCATTT 81
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Db      82  TTTATGTCCTTAGTAGCTTTTGTCTATTAATGCTAGGAAATGCTTTGGTCAATTTAGCTTT 141
Qy      121  GTGGTGACAGAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
Db      142  GTGGTGACAAAAACCTTTAGACATCGAAGTAGTTTATTTTCTTAACCTGGCCATCTCT 201
Qy      181  GACTTTCCTCGTGGGTTTGTATTTCCATTTCCCTCTGTACATCCCTCACGTGTTGTTAACTGG 240
Db      202  GACTTCTTTTGGGTGTGATCTCATTTCCCTTTGTACATCCCTCACGCTGTTTCAATGG 261
Qy      241  AATTTTGGAAAGTGAATCTGCATGTTTGGTCTCAATTAAGTACTGACTATCTTTTGTGACCCGA 300
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Qy      301  TCTGTCTACAAATATGTCTCATCTAGCTAGCATCGATACCACTGAGTTTCAAAATGCTGTG 360
Db      322  GCTGTATATAAGATTGTCTCATCAGCTATGATANAATACCTGTCAATCTCAAAATGCTTTG 381
Qy      361  TCTTATAGGGCTCAACACACTGGCATCATGAAGA 394
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RESULT 4
LOCUS   AK140374
DEFINITION Mus musculus adult male cortex cDNA, RIKEN full-length enriched
library, clone:R530005H20 product:h1stamine receptor H 3, full
insert sequence.
ACCESSION AK140374
VERSION    AK140374.1 GI:74150094
KEYWORDS   HTC; CAP trapper.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE
AUTHORS    Carninci, P. and Hayashizaki, Y.
TITLE      High-efficiency full-length cDNA cloning
JOURNAL    Meth. Enzymol. 303, 19-44 (1999)
PUBMED     10349636
REFERENCE 2
AUTHORS    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE      Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL    Genome Res. 10 (10), 1617-1630 (2000)
PUBMED     11042159
REFERENCE 3
AUTHORS    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kizumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE      RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL    Genome Res. 10 (11), 1757-1771 (2000)
PUBMED     11076861
REFERENCE 4
AUTHORS    Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakawa, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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```

Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, P., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Maehima, J., Mazzarelli, J., Mombauts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.

RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
11217851

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedziarski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y., Tlohm, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

FANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420 (6915), 563-573 (2002)  
1246851

6

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Banks, M., Baxter, L., Belsel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagioli, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huminicki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kello, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Luoni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuura, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G.,

Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sincalari, B., Sperling, S., Stupka, E., Sugiyama, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Bruscia, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

FANTOM Consortium

The transcriptional landscape of the mammalian genome  
Science 309 (5740), 1559-1563 (2005)  
16141072

7

Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.

RIKEN Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome  
Science 309 (5740), 1564-1566 (2005)  
16141073

8 (bases 1 to 2625)

Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Inotani, K., Itoh, M., Kangawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.

Location/Qualifiers

1. 2625

/organism="Mus musculus"

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/db\_xref="taxon:10090"

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/sex="male"

/tissue\_type="cortex"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="adult"

379, 1599

/note="unnamed protein product; histamine receptor H 3 (MGD|WGI:2139279 GB|NM\_133849, evidence: BLASTN, 99%, match=2436)

putative"

/codon\_start=1

CDS

FEATURES

source

COMMENT

TITLE

JOURNAL

REFERENCE

AUTHORS

CONSTRM

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

CONSTRM

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS



/protein\_id="BAE24362.1"  
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/translation="MGWLLIVAKVLGNALVMLAFVADSSLRTOHFFLLNLAIISDFLV  
GAFICPLVYPIVLTGRTWFGRLCKLWVVDYLLCASSVFNILVLSYDFLSVTVAVS  
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polya\_signal  
2602..2607

Query Match 12.0%; Score 140.8; DB 6; Length 2625;  
Best Local Similarity 55.9%; Pred. No. 1.5e-23;  
Matches 312; Conservative 0; Mismatches 237; Indels 9; Gaps 2;  
  
QY 78 CTTTGGCTAATAGTAGGCAATGCTGGTGCATCTTAGCCCTTTGTGGTGACAGAAACCT 137  
DB 396 CGTGGCCAAAGTCTGGGCAACGGCTGTCTGCTGCCTTCTGGGGGATTCGAGCCT 455  
  
QY 138 TAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCTGACTTCCTCGTGGGTTT 197  
DB 456 CCGCACCAGCAGCAACTCTTCTGCTCAACTCGCCATCTCCGACTTCCTGGTGGTGC 515  
  
QY 198 GATTTCAATCTCTGTACATCCCTCAGCTGTGTTTAAAC---TGGAAATTTGGAAGTGG 254  
DB 516 CTTCTGCATCCCAATTTATGTACCTATGTCTGACCGCGCGTTGGACCTTTGGCCGGGG 575  
  
QY 255 AATCTGCATGTTTGGCTCAATTAAGTACTATCTTTGTGACCGCATCTGTCTACAATAT 314  
DB 576 CTTCTGCAAGCTGTGGCTGGTGTAGTACTACTACTGTGCTCTCTCAGTCTTCAACAT 635  
  
QY 315 TGTCTCATTTAGTACGATCGATACCAAGTCAAGTTCAGTTTCAAAATGCTGTCTTATAGGGTCA 374  
DB 636 CGTCTCATCAGCTATGACGATTCCTGTGCTGAGTCACTCGAGCTGTCTCTACCGGGCCCA 695  
  
QY 375 ACACACTGGCATCATGAAGATTGTTGCTCAATAGTGGCTGTTTGGATATCTGGCTTCTT 434  
DB 696 GCAGGGGGACACAGACGGGCTGTTCGGAAGATGGCACTGGTGTGGGTGCTGGCTTCTCT 755  
  
QY 435 GGTAATAGGGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACACGACGACACAAAGG- 493  
DB 756 GCTGTATGGGCTGCCATCTCTGAGTGGGAGTACTGTCCGGTGGCAGCTCCATCCCCGA 815  
  
QY 494 -----ACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCCTACCAATTAACAATGCTCTT 548  
DB 816 GGGCCACTGCTATGCTGAGTCTTCTTCAACTGCTACTTTCTCATCGGCTCCACCT 875  
  
QY 549 GGAATTCCTGCTCTGCTGATCTCTGCTGGCTATTTCAATGTACAGATTTACTGGAGCCT 608  
DB 876 CGAGTCTCTTACACACCTTCTCTCAGCGTTACCTTCTCAACCTCAGCATCTACCTGAACAT 935  
  
QY 609 GTGGAACGGTAGGGCTCT 626  
DB 936 CCAGAGCGCACTCGTCT 953

RESULT 5  
DW582260  
LOCUS  
DEFINITION  
EST\_salal\_rgb2\_46679\_rgb2\_Salmo\_salar\_cDNA\_clone EST 17-JAN-2006  
salal\_rgb2\_575\_176\_rev\_5', mRNA sequence.  
DW582260  
VERSION  
DW582260.1 GI:85054082  
KEYWORDS  
EST.  
SOURCE  
Salmo salar (Atlantic salmon)

ORGANISM  
Salmo salar  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
1 (bases 1 to 791).  
REFERENCE  
AUTHORS  
Koop,B.F., Davidson,W.S. and cGRASP Consortium.  
Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)  
TITLE

JOURNAL  
COMMENT  
Unpublished (2006)  
Contact: Koop BF  
Centre for Biomedical Research  
University of Victoria  
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
Tel: 250 472 4067  
Fax: 250 472 4075  
Email: bkoop@uvic.ca  
Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.  
Marra, Bioinformatics Centre for Biomedical Research, University  
of Victoria Jong Leong, BF Koop.  
Insert Length: 791 Std Error: 0.00  
Plate: 575  
Seq primer: M13 Reverse  
High quality sequence stop: 791.  
Location/Qualifiers  
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/tissue\_type="mixed tissue"  
/clone\_lib="rgb2"  
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ssalrgb2 mixed tissue Salmo salar cDNA; Tissue  
contributors: Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN  
Query Match 11.8%; Score 139; DB 10; Length 791;  
Best Local Similarity 59.1%; Pred. No. 3.1e-29;  
Matches 257; Conservative 0; Mismatches 175; Indels 3; Gaps 1;  
  
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QY 81 TGCTATTAATGGTAGGCAATGCTGTGCTCATCTTAGCCTTTTGTGGTGACAGAAACCTTAG 140  
DB 279 CGCCACTGTGCTAGGCAACCGCTTGTAACTAGTACCTTTTGGGTGGAGAAAGTTTGGC 338  
  
QY 141 ACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCTGACTTCTCGTGGGTTTGTAT 200  
DB 339 AACTCAAGGAACCTTTTCTTTTGAATTTGGCCATAGCCGATTTACTCGTGGAGGTTT 398  
  
QY 201 TTCCATTTCTCTGTACATCCCTCACGCTGTT---GTTTAACTGGAAATTTTGGAACTGGAAT 257  
DB 399 TTGTTATTCGGTTTATATCCCTATGTCTATCCGGGAGTGGAGACTCGGACGAGGTCT 458  
  
QY 258 CTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCAACCGCATCTGTCTACAATTTGT 317  
DB 459 TTGCAAGATATGGTGGTGGGACTATATCTTTATGCACTGCATCAGTGTTCACATCGT 518  
  
QY 318 CCTCATTTAGCTACGATCGATACCACTCAGTTTCAAATGCTGTGCTTATAGGGCTCAACA 377  
DB 519 CCTGATCAGCTTCGACAGATTTATATCTGTCAACAAGCGGTAGCTACAGGTGTCAAG 578  
  
QY 378 CACTGGCATCATGAAGATTTGCTCAAATGGTGGCTGTTTGGATACTGGCTTTCTTGGT 437  
DB 579 AGGTGTGACCGGGAGGCTGTTCTGAAGATGATGAGTGTGGCTGCTTCTTCTACT 638  
  
QY 438 AATATGGCCCGATGAT 452  
DB 639 CTATGGGCCAGCGAT 653

RESULT 6  
CB556920  
LOCUS  
DEFINITION  
CB556920  
CB556920  
CB556920.1 GI:29496320  
CB556920 672 bp mRNA linear EST 02-APR-2003  
AMGNNUC:URGP1-00001-D6-A urgp1 (14349) Rattus norvegicus cDNA clone  
urgp1-00001-d6 5', mRNA sequence.  
ACCESSION  
VERSION  
CB556920.1 GI:29496320

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KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
JOURNAL Sciurognathi; Muridae; Muridae; Murinae; Rattus.
COMMENT 1 (bases 1 to 672)
Angen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
FEATURES
source Location/Qualifiers
1. .672
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="urp1-00001-d6"
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/notes="Vector: pSPORT1; Rat GPCR library rearrayed
internal pSPORT vector"

ORIGIN
Query Match 11.5%; Score 135.8; DB 4; Length 672;
Best Local Similarity 57.2%; Pred. No. 2.6e-28;
Matches 267; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

QY 3 GTCCGAGTCTAACAGTACTGGCATCTGGCCACGAGTGTCTCAGTCCCTCCCTGGCATTTT 62
DB 178 GCGGGTGTGAGCGGGGGCGGGCTCTCGGCTGTCTGACCGCTGTCTGCTGGCT 237
QY 63 AATGTCTTCAATTTGCTTATATAGTGGAGCAATGTCTGCTCATCTTACCTTTGT 122
DB 238 CATGGGCTCTCATCTGTGCCACAGTACTGGGCAAGCGCTGTCTATGCTCGCTTGT 297
QY 123 GGTGGACAGAACTTAGACATCGAAGTAAATTTTCTTAAATTTGGCTATTCTGA 182
DB 298 GCGGGATTCGAGCTTCGGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGA 357
QY 183 CTTCCTCTGGTGTGATTTCCATCTCTGTATACCTCCCTCAGTGTGTTTAACTG 239
DB 358 CTTCCTCTGGTGTGCTTCTGATTCATTCATCTGATACCTATGTCTGACCGCGT 417
QY 240 GAATTTTGGAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCAAC 299
DB 418 GACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGGTAGACTACTCTGTTGCTC 477
QY 300 ATCTGTCTCAATTTGTCTCTATAGCTAGCATGATACCATCTGATTTCAATGCTGT 359
DB 478 CTCGGTCTTCAACATCGTACTCATGACTATGACCATTCCTGTGACTCTCGAGCTGT 537
QY 360 GTCTTATAGGCTCAACACCTGGCATCATGAGATTTGTTGCTCAATGGTGGCTTTG 419
DB 538 CTCTACAGGGCCAGCAGGGGACAGAGACGGCGGCTTCGGAAGATGCGACTGTGTG 597
QY 420 GATACCTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATT 466
DB 598 GGTGCTGGCTTCTCTGTGTATGGGCTGCCATCTCTGAGTTGGAGT 644

RESULT 7
LOCUS CF147822 732 bp mRNA linear EST 25-JUL-2003
DEFINITION AGENCOURT 14740187 NIH MGC 145 Homo sapiens cDNA clone
IMAGE:6971899 5', mRNA sequence.
ACCESSION CF147822
VERSION CF147822.1 GI:33244090
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
```

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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
COMMENT 1 (bases 1 to 732)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB102 row: b column: 06
High quality sequence stop: 610.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971899"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="NIH MGC 145"
/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 11.4%; Score 133.8; DB 5; Length 732;
Best Local Similarity 53.5%; Pred. No. 1.1e-27;
Matches 329; Conservative 0; Mismatches 277; Indels 9; Gaps 2;

QY 3 GTCCGAGTCTAACAGTACTGGCATCTTGGCACAGCTGTCTCAGTCCCTCCCTGGCATTTT 62
DB 76 GCGCGCGCGGGCGGGCGCGGCTTCTCGGACGCTTGGACCGGTGCTGGCGCGCT 135
QY 63 AATGTCTTCAATTTGCTTATATAGTGGAGCAATGTCTGCTCATCTTAGCTTTGT 122
DB 136 CATGGCGTCTCATCTGTGGCACGGTGTGGGCAAGCGCTGTATGCTCGCTTCGT 195
QY 123 GGTGGACAGAACTTAGACATCGAAGTAAATTTTCTTAAATTTGGCTATTCTGA 182
DB 196 GCGCGACTCGAGCTTCGGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGA 255
QY 183 CTTCCTCTGGTGTGATTTTCAATCTCTGTATACCTCCCTCAGCTGTG---TTTAACTG 239
DB 256 CTTCCTCTGGCGGCTTCTGCAATCCCACTGTATGACCTAGCTGTGACAGCGCGCTG 315
QY 240 GAATTTTGGAGTGAATCTGCATGTTTGGCTCAATTACTGACTATCTTTGTGCAACCG 299
DB 316 GACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTGCTGTGCACCTC 375
QY 300 ATCTGTCTCAATTTGTCTCTATAGCTAGCATGATACCATCTGATTTCAATGCTGT 359
DB 376 CTCTGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTCTGCTGCTACCGAGCGGT 435
QY 360 GTCTTATAGGCTCAACACATCGGCAATCATGAGATTTGTGCTCAATGCTGGCTGTTG 419
DB 436 CTCAATACCGGGCCAGCAGGGTGACACGGCGCGGCGAGTGCGGAAGATGCTGTGGTGTG 495
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QY 420 GATACGCTTCTCTGTAATGCGCCGATGATCTCGCTTCAGA-----TTCTTGAA 473  
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 QY 534 CATTACAATGCTCTTTGAAATCTCTGCTTCTCTGTCATCTCTGTGGCTTATTTCAATGACA 593  
 Db 616 CACGGCTTCCCACTGAGTCTTTACGCCCTTCTCAGCGCTCTCTCAGCGTCACTTTCTTTAACTCTAC 675  
 QY 594 GATTACTGAGGCT 608  
 Db 676 CATCTACCTGAACAT 690

## RESULT 8

DT257276

LOCUS DT257276 728 bp mRNA linear EST 18-AUG-2005  
 DEFINITION JGI\_CAAU8039.fwd CAAU Pimephales promelas brain 7-8 month adults, males and females pooled (L) Pimephales promelas cDNA clone CAAU8039 5', mRNA sequence.

ACCESSION DT257276.1 GI:73559225

VERSION EST.

KEYWORDS Pimephales promelas

SOURCE Pimephales promelas

ORGANISM Pimephales promelas

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Pimephales.

1. (bases 1 to 728)

Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C.,

Brokstein, P. and Lindquist, E.A.

DOE Joint Genome Institute Pimephales promelas EST project

Unpublished (2005)

Other\_ESTs: JGI\_CAAU8039.rev

Contact: Lindquist, E.A., Richardson, P.

DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 296 5600

Fax: 925 296 5710

Email: cdna@jgi-psf.org

cDNA Library Preparation: DOE Joint Genome Institute:

http://www.jgi.doe.gov

DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.

Plate: CAAU 0081 row: n column: 18

High quality sequence stop: 706.

## FEATURES

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 /tissue\_type="brain"  
 /clone\_lib="CAAU Pimephales promelas brain 7-8 month adults, males and females pooled (L)"  
 /notes="vector: pCMVSPORT6; The library was made from dt primed cDNA and cloned into Invitrogen vector pCMVSPORT6. Poly A RNA were primed with an oligo dt primer (5'-GACTACTCTAGATCGAGCGCGCCCTTTTCTTTT-3') ligated to a SalI adapter (5'-TCGACCCAGCGCCG and 5'-CGACCGTGGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L -0.5-1.2k, M -1.2-2.5k, H ->2.5k) then ligated into NotI and SalI digested pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute."

## ORIGIN

Research Association for Biotechnology (RAB) and Biotechnology

Query Match 11.1%; Score 130.2; DB 10; Length 728;  
 Best Local Similarity 57.3%; Pred. No. 1.2e-26;  
 Matches 256; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

QY 21 TGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCATTTTAAATGCTTTCATTTCGCTT 80

Db 256 TGGCCAGTTTACTCCATCCACCTCAATATTCCTGACAGTTCTCATGACACTGCTGTGT 315

QY 81 TGTATTAATGGTAGGCAATGCTGTGGTCACTCTTAGCCTTTGTGTGGTGGACAGAAACCTTAG 140

Db 316 CGCACCGTTCTCGGGAACGCGTTGTCAITTTAGCTTTTGTGTGGTGGAGAAAGTTTACG 375

QY 141 ACATCGAAGTAATATTTTCTTAAATTTGGCTATTTCTGACTTCTCTCGTGGGTTTGCAT 200

Db 376 CACAAAGGCAACTTTTCTTTTAAATTTGGCCATAGCGGACTTTCTTGTGCGTGGTT 435

QY 201 TTCCATTCTCTGTACATCCC--TCACGTGTTGTTTAACTGGAAATTTTGGAACTGGAAT 257

Db 436 TTGCATCCCGTGTATATTCCTATGTCCTGACGGGTGAGTGGAGGCTGGGCAGAGTCT 495

QY 258 CTGCATGTTTGGTCAATTAATGACTATCTTTTGTGCAACGCGATCTGTCTACAATATTGT 317

Db 496 GTGTAAACTGTGGCTGGTAGTGGATTACATGTTGTGCACCTGCCTCAGTCTTCAACATCGT 555

QY 318 CCTCATTTAGCTAGATCGATACCATGACAGTTCAGTTTCAAAATGCTGTCTTATAGGGCTCAACA 377

Db 556 GCTCATCAGTTTCGACAGGTTTCAGTCCGTCACATAAGCGGTGAGTTACCATTCGCCAAA 615

QY 378 CACTGGCATCATGAAGATTGTCCTCAATGGTGGCTGTTTGGATATCTGGCTTCTTCTGGT 437

Db 616 GGGATCACCAGAGAGGCTGTTTGAAGATGCTCTGTGTGGCTTCGACGGTTCCTTCT 675

QY 438 AAATGGCCCCGATGATTCTGGCTTCAGA 464

Db 676 TTAATGGTCCAGCATATTCAGTTGGGA 702

RESULT 9

DA308555 BRHIP2 Homo sapiens cDNA clone BRHIP2025783 5', mRNA

LOCUS DA308555 558 bp mRNA linear EST 30-OCT-2005

DEFINITION DA308555 BRHIP2 Homo sapiens cDNA clone BRHIP2025783 5', mRNA

ACCESSION DA308555

VERSION DA308555.1 GI:78290625

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1. (bases 1 to 558)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

1634560

Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction;

Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

## FEATURES

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## ORIGIN

Query Match 11.0%; Score 129.2; DB 9; Length 558;  
Best Local Similarity 55.5%; Pred. No. 2.2e-26;  
Matches 295; Conservative 0; Mismatches 228; Indels 9; Gaps 2;  
QY 53 TGCATTTTAAATGCTCTTCAATTTGGCTTTGCTATAATGGTAGCAATGCTGTGCTCATCT 112  
Db |||||  
QY 27 TGCGCGGCTCATGGCGTCTCATCTGCGCCACGGTGTGGGCAACGGCTGGTCATGC 86  
Db |||||  
QY 113 TAGCCTTTGTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGG 172  
Db |||||  
QY 87 TCGCCTTGTGGCGGACTCGAGGCTCGGCACCGAACAACCTTCTTCTGCTCAACCTCG 146  
QY 173 CTATTTCTGACTTCTCTGCGGTTTGATTTCCATCTCTGTACATCCCTCACGTTGTG- 231  
Db |||||  
QY 147 CCACTCTCGGACTTCTCTGCTCGGCGCTTCTGCATCCCACTGTATGTACCTAGTCTGA 206  
QY 232 --TTTAACTGGAATTTTGAAGTGGATCTGCATCTTTTGGCTCATTTACTGACTATCTTT 289  
Db |||||  
QY 207 CAGCGCGCTGACCTTCGCGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTACCTGC 266  
QY 290 TGTGACCGCATCTGTCTACAATATTGTCTCTATTTAGTACGATCGATACGATCAGTTT 349  
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QY 267 TGTGCACTCTCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTCTCGGTCA 326  
QY 350 CAAATGCTGTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGG 409  
Db |||||  
QY 327 CCGAGCGGTCTCATACCGGGGCCAGCAGGGTGACACGGCGGGGAGTCCGGAAGATGC 386  
QY 410 TGCGTGTGGTACTGGCTTCTTGTGTAATAGCCCGATGATCTGGCTTCAGA----- 464  
Db |||||  
QY 387 TGTGTTGTGGTGTGGCTTCTCTGTGTACGACACCGCATCTGAGCTGGAGTACC 446  
QY 465 -TTCTTGAAGAACAGCACAAACAAAGACATGTGAGCCTGCTTGTTCAGAGTGGT 523  
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QY 447 TGTCCGGGGGACGCTCCATCCCGGAGGCGCACTGCTATGCCGAGTTCTTCTACAACTGGT 506  
QY 524 ACATCTCTCACCATTAAGTCTCTTGGAAATTCCTGCTTCTGTCATCTCTGT 575  
Db |||||  
QY 507 ACTTCTCTCATCGGGCTTCCACCTGGAGTTCTTTAGCGCCCTTCTCAGCGT 558

## RESULT 10

CD326085 853 bp mRNA linear EST 28-MAY-2003  
LOCUS  
DEFINITION  
AGENCOURT 14163426 NICHD\_XGC\_Eyel Xenopus laevis cDNA clone  
IMAGE:6949081 5', mRNA sequence.

## ACCESSION

CD326085

## VERSION

CD326085.1 GI:31090416

## KEYWORDS

EST.

## SOURCE

Xenopus laevis (African clawed frog)

## ORGANISM

Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 853)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics

National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement:

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.llnl.gov>  
Plate: LLAM14564 row: f column: 24  
High quality sequence stop: 707.

## FEATURES

Location/Qualifiers  
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/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:6949081"  
/dev\_stage="adult"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NICHD\_XGC\_Eyel"  
/note="Organ: eye; Vector: pCMV-SPORT6; Site:1: NotI;  
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: This is a Xenopus Gene Collection  
(XGC) library."

## ORIGIN

Query Match 11.0%; Score 129.2; DB 5; Length 853;  
Best Local Similarity 58.7%; Pred. No. 2.6e-26;  
Matches 243; Conservative 0; Mismatches 168; Indels 3; Gaps 1;  
QY 45 GGTCCTCTGGCATTTTAAATGCTTTCATTTGCTTATTAATGTTAGGCAATGCTGT 104  
Db |||||  
QY 381 GGTCTCTCTGGCTGCTCTGATGGGGTCTCTAGTTAGCACCGTCTGGGGAATGCCCT 440  
QY 105 GGTCACTCTTAGCCCTTTGTGTGGACAGAAACCTTAGACATCGAAGTAATTTTCT 164  
Db |||||  
QY 441 GGTCACTGCTGGCTTTTGTGTGGACTCCAGCTCCGAAACCCAGAAATTTCTCTCTCT 500  
QY 165 TAAATTTGGCTATTTCGACTTCTCTGTTGGTTTGAATTTCCATTCCTCTGATCCCTCA 224  
Db |||||  
QY 501 CAACCTGGCTATCTCAGATTTCTTTGTAGTGGCTGTGCATCCCTCTGATGTGCCATA 560  
QY 225 CGGTGTTGTTT---AATCGAAATTTGGAAGTGAATCTGCATGTTTGGCTCAATCTGA 281  
Db |||||  
QY 561 CGTACTGACTGGCAGATGGAGCTTTGGCAGGAGCGTTTGAACACTGGCTGGTCTTCTGA 620  
QY 282 CTATCTTTTGTGACCGCATCTCTCTACAAATATTTGCTCTATTAGTCTACATGATACCA 341  
Db |||||  
QY 621 TTAATCTGCTGCACCTCGTCCGTGTTCAACATCGTGTCTCATCAGCTACGACAGTTTCT 680  
QY 342 GTCACTTTCAATGCTGTGCTTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTC 401  
Db |||||  
QY 681 CTCTGTGACCCGGGCTGTCTAGTTACCAGCTCAGCAGAGTAACACCGCGCATGCAGTCTT 740  
QY 402 TCAAAATGGTGGCTTTTGGATCTGCTTTTGGTAAATGGCCGATGTTCT 455  
Db |||||  
QY 741 GAAATGACCATGGTGTGGATCTTTGGCTTTTCTTATATATGACCGCATTTAT 794

## RESULT 11

## LOCUS

DW576242

## DEFINITION

EST\_ssal\_rgb2\_40661\_rgb2 Salmo salar cDNA clone

ssal\_rgb2\_566\_015\_rev 5', mRNA sequence.

## ACCESSION

DW576242

## VERSION

DW576242.1 GI:85048064

## KEYWORDS

EST.

## SOURCE

Salmo salar (Atlantic salmon)

## ORGANISM

Salmo salar  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;

```

REFERENCE
AUTHORS      Koop,B.F., Davidson,W.S. and cGRASP Consortium.
TITLE        Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
JOURNAL      Unpublished (2006)
COMMENT      Contact: Koop BF
              Centre for Biomedical Research
              University of Victoria
              PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
              Tel: 250 472 4067
              Fax: 250 472 4075
              Email: bkoop@uvic.ca
              Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.
              Marra. Bioinformatics: Centre for Biomedical Research, University
              of Victoria Jong Leong, BF Koop.
              Insert Length: 542 Std Error: 0.00
              Plate: 566
              Seq primer: M13 Reverse
              High quality sequence stop: 542.

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source       Location/Qualifiers
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/organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
/db_xref="taxon:8030"
/clone="ssal_igb2_566_015_rev"
/tissue_type="mixed tissue"
/notes="Organ: brain, kidney, spleen; Vector: pCMVspout6;
ssalqib2 mixed tissue Salmo salar cDNA; Tissue
contributors: Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN
Query Match      10.8%; Score 126.8; DB 10; Length 542;
Best Local Similarity 56.5%; Pred. No. 1.1e-25;
Matches 280; Conservative 0; Mismatches 207; Indels 9; Gaps 2;

QY 133 AACCTTAGACATCGAAGTAATATTTTTCCTTAATTTGGCTATATTCGACTCTCTCGTG 192
DB 1 AGCCTACGAATCAAAGCAACTACTTCTCTCAACCTTGCCATTTTCAGATTTTCTTGTT 60

QY 193 GGTTTGATTTCCATCTCTGTACATCCCTCAGTGTGTTTAA---CTGGAATTTTGA 249
DB 61 GGTGCAATCTGTATCCCTGTATACATCCCTCAACCTGACAGCCGCTGGGTGCTGGC 120

QY 250 AGTGGAAATCGCATGTTTGGCTCATTAAGTACTATCTTTTGTGCACCGCATCTGTCTAC 309
DB 121 AGAGGTCTCTGAAGCTGTGGCTCCTCATGACTACTTGTCTGCACTGGCTGTGCTTC 180

QY 310 AATATTGTCTCTAATAGTACGATCGATACAGTCAGTTCCTCTCCGTCACAGAGCAGTGAAATATAGA 240
DB 181 AACATAGTCTCTATCAGCTATGACCGGTTCTCTCCGTCACAGAGCAGTGAAATATAGA 240

QY 370 GCTCAACACTGGCATCATGAAGATTTGTTGCTCAATGTGGCTGTTTGATCTGGCT 429
DB 241 GCTCAGCGGAGCATGACCCCACTGCTGTGTGAAGATGTGTGGCTGTGTGGCT 300

QY 430 TTCTTGTAATAGCCCGGATTTCT-----GCCTTCAGATTTCTTGGGAAGAACAGCAGC 483
DB 301 TTCTTCTCTATGGCCCTGCGCATTAUCTTCTGGAGCTGTTGTGGGTAAAGCATCGTT 360

QY 484 AACACAAGACTGTGAGCCGTGGCTTTGTTTACAGAGTGGTATACCTTCACCATTTACAATG 543
DB 361 CCTGCCGACAGTGTTCGCTGAGTCTTACTGCACCTGGTACTTCTCTACTCAGTGGCTCT 420

QY 544 CTCTTGAATTCCTGCTTCTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTACTGG 603
DB 421 ACGTTTGAGTTCTTCAACCCCTTTATCTCTGTGACCTTCTTCAACCTGTGCTATCTACCTG 480

QY 604 AGCTGTGGAGCGTA 619
DB 481 AACATCCAGAGGAGGA 496

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RESULT 12
CC481311
LOCUS    CH240_309C10.T7 CHORI-240 Bos taurus genomic clone CH240_309C10,
DEFINITION genomic survey sequence.
ACCESSION CC481311
VERSION    CC481311.1 GI:31760574
KEYWORDS   GSS.
SOURCE     Bos taurus (cattle)
ORGANISM   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 684)
AUTHORS   Holt,R., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
          Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
          Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
          Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
          Dalrymple,B.P. and Tellam,R.
          Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
          Unpublished (2003)
          Other GSSs: CH240_309C10.TARBAC13P2
          Contact: Rob Holt
          Sequencing
          The British Columbia Cancer Agency Genome Science Centre
          600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
          Tel: 604-877-6085
          Fax: 604-877-6276
          Email: rholt@bcgsc.ca
          Clones are derived from the bovine BAC library CHORI-240
          (http://www.chori.org/bacpac/bovine240.htm). For BAC library
          availability, please contact Pieter de Jong (pjejong@mail.choi.org).
          Clones may be purchased from BACPAC Resources
          (http://www.chori.org/bacpac/ordering/information.htm). This work
          was undertaken as part of the International Bovine BAC Mapping
          Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
          British Columbia Genome Sciences Centre, Canada.
          Plate: 309 row: C column: 10
          Seq primer: T7
          Class: BAC ends.

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/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_309C10"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match      9.8%; Score 115.6; DB 12; Length 684;
Best Local Similarity 70.6%; Pred. No. 2.6e-22;
Matches 154; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 150 TAATATTTTTCCTTAATTTGGCTATTTCTGACTTCTCTCGTGGTGTGATTTCCATTCC 209
DB 260 TACGTGCTATATTGTTTAATCTTCAUATTTTTCGCCCATGCGAGTATGATCTCCATTCC 319

QY 210 TCTGTACATCCCTCAGCTGTGTTTAACTGGAATTTTGGAGTGGATTCGATGTTTG 269
DB 320 TTTATTATCCCTCCACAAGCTCTTCAACTGGAGTTTGAATAAACAATTTGTGTCTTTG 379

QY 270 GCTCATTACTGACTATCTTTTGTGCACCGCATCTGTCTACAATATTGTCCTCATTAGCTA 329
DB 380 GCTCATTACTGACTATCTTTTGTGTGACGATCTGTGTATAACATCGTACTCATCAGCTT 439

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QY      330 CGATCGATACCACTGCTAGTTTCAAATGCTGTGCTTATTA 367
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Db      440 TGAATGATATCACTGCTAGTCTCCAATGCTGTAAGTCAA 477

RESULT 13
LOCUS   DA306992
DEFINITION DA306992 BRHIP2 Homo sapiens cDNA clone BRHIP2023706 5', mRNA
          574 bp mRNA linear EST 28-OCT-2005
ACCESSION DA306992
VERSION    DA306992.1 GI:78244614
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE 1 (bases 1 to 574)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
           Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
           Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
           Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
           Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
           Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
           Diversification of Transcriptional Modulation: Large-scale
           Identification and Characterization of Putative Alternative
           Promoters of Human Genes
           Genome Res. 16 (1), 55-65 (2006)
JOURNAL   16344560
PUBMED    Contact: Takao Isogai
COMMENT    FLJ Project (HRI Team)
           Helix Research Institute
           2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
           Tel: 81-438-52-3975
           Fax: 81-438-52-3986
           Email: flj-cdn@nifty.com
           NEDO human cDNA project (New Energy and Industrial Technology
           Developmental Organization, Japan); cDNA library construction:
           Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
           Research Association for Biotechnology (RAB) and Biotechnology
           Center, National Institute of Technology and Evaluation; 3'-end one
           pass sequencing: RAB.
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Best Local Similarity 55.1%; Pred. No. 7.3e-22;
Matches 269; Conservative 0; Mismatches 210; Indels 9; Gaps 2;

QY      151 AATATATTTTCTTAATTGGCTATTTCTGACTTCTCTGTGGTTTGATTCATTCCT 210
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Db      16  AACTTCTCTCGTCAACCTCGGCATCTCCGACTCTCCGTGCGGCCCTTCTGCATCCCA 75

QY      211 CTGTACATCCCTCAGCTGTGTTTAAAC--TGGAAATTTTGGAAAGTGAATCTGCATGTTT 267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      76  CTGTATGATACCTACGTGCTGACAGCGCTGGACCTTCGGCCGGGCGCTCTGCAAGCTG 135

QY      268 TGGCTCATTTACTGACTATCTTTTGTGCACCGCATCTGTCTTACAAATATGTCCTCATTAGC 327
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      136 TGGCTGTGTAGTGACTACCTGCTGTGCACCTCTCTGCTTCAACATCGTGTCTCATCAGC 195

QY      328 TAGCATCGATACAGTCAGTTTCAATATGCTGTGTCTTATAGGGCTCAACACATGGCATC 387
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Db      196 TAGACCGCTTCTGTGCGTCAACCGGCGGTCTCATACCGGCGCCCGAGGGGTGACAG 255

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QY      388 ATGAAGATTGTTGCTCAAAATGGTGGCTGTTTGGATACTGGCTTTCTTGGTAAATGGCCCG 447
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Db      256 CGCGCGGCGAGTGGGAAGATGCTGTGGTGTGGGTGCTGGCCCTTCTCTGTGTACGGACCA 315

QY      448 ATGAATTCGTGGCTTCAGA-----TTCTTGGAGAAGACAGACAGAACAAAGGACTGTGAG 501
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      316 GCCATCTTCAGCTGGGAGTACCTGTCCGGGGGCGAGCTCCATCCCGAGGCGCCACTGCTAT 375

QY      502 CCTGGGCTTGTGTACACAGTGGTACATCTCACCATTAACAATGCTCTTGGAAATTCCTGCTT 561
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      376 GCCGAGTTCTTACAACTGGTACTTCTCCATCACCGCTTCCACCTTGGAGTTCTTTACG 435

QY      562 CCTGTCAATCTCTGTGGCTTATTTTCAATGTACAGATTTACTGGAGCCTGTGGAAAGCGTAGG 621
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      436 CCCTTCCTCAGCGTCACCTCTTTTAACCTCAGCATCTACCTGAACATCCAGAGGCGCACC 495

QY      622 GCTCTCAG 629
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Db      496 CGCCTCCG 503

RESULT 14
LOCUS   DA728518
DEFINITION DA728518 NT2RM2 Homo sapiens cDNA clone NT2RM2001941 5', mRNA
          755 bp mRNA linear EST 11-NOV-2005
ACCESSION DA728518
VERSION    DA728518.1 GI:81799719
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE 1 (bases 1 to 755)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
           Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
           Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
           Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
           Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Sugano,S.
           Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
           Diversification of Transcriptional Modulation: Large-scale
           Identification and Characterization of Putative Alternative
           Promoters of Human Genes
           Genome Res. 16 (1), 55-65 (2006)
JOURNAL   16344560
PUBMED    Contact: Takao Isogai
COMMENT    FLJ Project (HRI Team)
           Helix Research Institute
           2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
           Tel: 81-438-52-3975
           Fax: 81-438-52-3986
           Email: flj-cdn@nifty.com
           HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
           Research Institute (HRI); cDNA library construction: Department of
           Virology, Institute of Medical Science, University of Tokyo, and
           HRI.
FEATURES
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Best Local Similarity 55.0%; Pred. No. 1.9e-19;

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1 ATCTCCGACTTCTCTCGTGGCGCTCTCTGCAATCCCACTGTATGATACCTACGTCGTGACA 60
Qy 232 TTTAACTGGAAATTTGGAAGTGAATCTGCAATGTTGGCTCATCTACTGACTATCTTTTG 291
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 GCGCGCTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGAGTACTCTGCTG 120
Qy 292 TGCACCGCATCTGCTCAATATTTGCTCTATTAGTACGATCGATACCACTGATGTTTCA 351
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 TGCACCTCTCTGCTTCAACATCTGTCCTCACTAGTACGACCTCTCTCTGCTGCTGTCACC 180
Qy 352 AATCTGTGCTTATAGGCTCAACACACTGGCATCATGAAGATGTTGCTCAAAATGGTG 411
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 CGAGCGGTCTCATACCGGGCCAGCAGGGTGACACGGCGGGCGAGTGCAGGAAGATGCTG 240
Qy 412 GCTGTTGGATACGCTTCTTGGTAAATGCGCGATGATTCCTGGCTTCAGA-----T 465
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 CTGGTGTGGGTGCTGGGCTTCTCTGCTGTACGGACCAATCTCTGAGCTGGGAGTACCTG 300
Qy 466 TCTTGAAGAACACACACACAAAGGACTGTGAGCTGCTGCTTGTACAGAGTGGTAC 525
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 TCCGGGGCAGCTCTCATCCCGAGGGCAGTCTGTATGCCGAGTCTTCTTACAACTGGTAC 360
Qy 526 ATCTCTACCAATACAAATGCTCTTGGAAATCTGCTTCTCTGTCATCTCTGTGGCTTATTTC 585
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 TTCCTCATCGGCTTCCACCTGGAGTCTTTACGGCCCTTCTCAGCGTCACCTCTTTT 420
Qy 586 AATGTACAGATTACTGAGGCTGTGAGGCTAGGAGCTCTCAG 629
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 AACCTGACATCTACCTGAACATCCAGAGGGCGCACCGGCTCCG 464
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RESULT 15  
DY313565  
LOCUS  
DEFINITION  
IMAGE:8317348 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 687)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
DNA sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRB110 row: c column: 02  
High quality sequence stop: 252.  
Location/Qualifiers  
1. .687  
/organism="Homo sapiens"  
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FEATURES  
source

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pcDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',  
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clone represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat  
a Note: this is a NIH_MGC Library."  
  
ORIGIN  
Query Match 8.6%; Score 101.2; DB 10; Length 687;  
Best Local Similarity 56.1%; Pred. No. 5e-18;  
Matches 212; Conservative 0; Mismatches 163; Indels 3; Gaps 1;  
  
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66 GCGCGCGCGCGCGCGCGCGCTTCTCGGAGCTGGACCGGCTGCTGGCGCGCT 125  
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
126 CATGGCGCTGCTCATCTGTCACGCTGCTGGGCAACGCGCTGCTCATGCTCGCTTCGT 185  
Qy 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182  
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186 GCGCGACTCGAGCTCCGCGACCCAGAACAACTTCTCTGCTCAACCTCGCTACTCCGA 245  
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246 CTTCCTCTGCTGAGCGCTTCTGTCATCCCTCTGTATGTACCTTACCGCGCGCTG 305  
Qy 240 GAATTTTGGAGTGAATCTGTCATGTTTGGCTCATTTACTGACTATCTTTTGTGACCGC 299  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
306 GACCTTCGCGCGCGCTCTGCAAGCTGTGCTGTAATGGAATACCTGATGTGCACATC 365  
Qy 300 ATCTGCTCTACAATATTTGCTCTCATTTAGCTAGCATCGATACAGTCAGTTTCAAAATGCTGT 359  
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366 ATCAGCCTTCAAAATCGGCGCATCAGCTAGGAAGAAATTTCTGTCCGATACACAAGCAGT 425  
Qy 360 GTCTTTAGGGCTCAACA 377  
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426 CACATACAGGTCACGCA 443
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Job time : 6437 secs





GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 21:02:08 ; Search time 263 Seconds  
(without alignments)  
8366.631 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

Sequence: 1 atctcgagctcaacagctac.....accagtcagtatcttttga 1176

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /EMC\_Celerra\_SID33/prodata/2/ina/1\_COMB.seq:\*
- 2: /EMC\_Celerra\_SID33/prodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SID33/prodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC\_Celerra\_SID33/prodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC\_Celerra\_SID33/prodata/2/ina/7\_COMB.seq:\*
- 6: /EMC\_Celerra\_SID33/prodata/2/ina/H\_COMB.seq:\*
- 7: /EMC\_Celerra\_SID33/prodata/2/ina/PCTUS\_COMB.seq:\*
- 8: /EMC\_Celerra\_SID33/prodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC\_Celerra\_SID33/prodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC\_Celerra\_SID33/prodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	686.6	58.4	1173	3	US-09-414-010-1
2	686.6	58.4	1173	3	US-09-812-216-1
3	686.6	58.4	1173	3	US-09-875-076-13
4	172.8	14.7	1239	3	US-09-891-053-2
5	172.8	14.7	2700	3	US-09-891-053-5
6	143.2	12.2	1338	3	US-09-165-543-6
7	143.2	12.2	1953	3	US-09-891-053-26
8	143.2	12.2	3244	3	US-09-165-543-4
9	140.4	11.9	1335	2	US-08-985-090-3
10	140.4	11.9	1335	3	US-09-165-543-3
11	140.4	11.9	1335	3	US-09-167-354-6
12	140.4	11.9	1335	3	US-09-642-855-6
13	140.4	11.9	1335	3	US-09-642-514-6
14	140.4	11.9	1335	3	US-09-642-852-6
15	140.4	11.9	2050	3	US-09-891-053-21
16	140.4	11.9	2685	3	US-09-949-016-5059
17	140.4	11.9	2689	2	US-08-985-090-1
18	140.4	11.9	2689	3	US-09-165-543-1
19	140.4	11.9	2699	3	US-09-167-354-5
20	140.4	11.9	2699	3	US-09-642-855-5
21	140.4	11.9	2699	3	US-09-642-514-5
22	140.4	11.9	2699	3	US-09-642-852-5
23	94	8.0	1086	2	US-08-985-090-6

24	94	8.0	1086	3	US-09-165-543-33	Sequence 33, Appli
25	94	8.0	2218	2	US-08-985-090-4	Sequence 4, Appli
26	94	8.0	2218	3	US-09-165-543-31	Sequence 31, Appli
27	93.8	8.0	1056	3	US-09-524-162-1	Sequence 1, Appli
28	72.6	6.2	1893	3	US-09-891-053-13	Sequence 13, Appli
29	72.6	6.2	9293	3	US-09-949-016-16801	Sequence 16801, A
30	72	6.1	601	3	US-09-949-016-177027	Sequence 177027,
31	67.6	5.7	1401	3	US-08-826-509-514	Sequence 514, App
32	67.6	5.7	1569	5	US-09-543-679A-2590	Sequence 2590, Ap
33	67.6	5.7	2210	3	US-09-016-434-1177	Sequence 1177, Ap
34	67.6	5.7	2210	3	US-10-166-199-1	Sequence 1, Appli
35	67.6	5.7	6707	5	US-09-543-679A-2593	Sequence 2593, Ap
36	64.4	5.5	1599	3	US-08-826-509-520	Sequence 520, App
37	64.4	5.5	2261	3	US-08-016-434-1176	Sequence 1176, Ap
38	61.6	5.2	448	3	US-09-891-053-12	Sequence 12, Appli
39	61.2	5.2	1233	3	US-09-721-870-176	Sequence 176, App
40	59	5.0	1773	3	US-09-826-509-516	Sequence 516, App
41	59	5.0	1913	3	US-09-016-434-1314	Sequence 1314, Ap
42	59	5.0	1913	5	US-09-543-679A-2592	Sequence 2592, Ap
43	57.6	4.9	1356	5	US-09-993-844A-12	Sequence 12, Appli
44	57.6	4.9	1579	3	US-09-016-434-1243	Sequence 1243, Ap
45	56.8	4.8	1440	3	US-09-826-509-518	Sequence 518, App

## ALIGNMENTS

RESULT 1  
US-09-414-010-1  
; Sequence 1, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monema, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-414-010-1

	Query Match	58.4%	Score 686.6;	DB 3;	Length 1173;
	Best Local Similarity	75.1%	Pred. No. 1.6e+201;		
	Matches	886;	Conservative	0;	Mismatches 284;
					Indels 9;
					Gaps 2;
Qy	1	ATGTCGAGTCTAACAGTACTGGCATCTTGCACAGCTGCTCAGTCCCTTGGCAATT	60		
Db	1	ATGCCAGATCTAATAGCACAAATTTATCTACTAGCACTCGTGTACTTTAGCACTTT	60		
Qy	61	TTAATGCTTCATTGCTTTGCTTATTAATGTTAGGCAATGCTGTGTCATCTTAGCCTTT	120		
Db	61	TTTATGTCCTTAGTAGCTTTTGTCTAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT	120		
Qy	121	GTGGTGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT	180		
Db	121	GTGGTGACAGAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCTATTCT	180		
Qy	181	GACTTCTCTGGGTTTGATTTTCATTCCTCTGTACATCCCTCACGCTGTTGTTAACTGG	240		
Db	181	GACTTCTTTTGGGTGTGATCTCCATTCCTTTTGTACATCCCTCACGCTGTTTGAATGG	240		
Qy	241	AATTTTGAAGTGAATCTGCATGTTTGGCTCACTACTATCTTTTGTGACCGCA	300		

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Db 301 TCTGTATATAACAAATGTCCTCATCGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGCTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACTGGGCTTGAAGATTTGATCTCTGAATGCTGGCTGTTGG 420
QY 421 ATACTGGCTTCTTGGTAATGAGCCGATGATCTGCTGCTTCAATTTCTGGAAGAACAGC 480
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QY 481 ACAGAACAAAGACTGTGAGCTGGCTTGTGTACAGAGTGGGTACATCTCCACCATTTACA 540
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## RESULT 2

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US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
```

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; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1
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Query Match 58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 1.6e-201;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCCGAGTCTAAACAGTACTGGCATCTTGCACCCAGCTGCTCAGGTCCCTTGGCAATTT 60
Db 1 ATCCGAGATCTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
QY 61 TTAATGTCTTCATTTGCCCTTGTCTATAAAGGTAGGCAATGCTGTGGTCACTCTTAGCCTTT 120
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QY 1141 CCAGCGCTGTACAGAAAC---CAGTCAATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACAGTGGCTGAGTATCTTCTTAA 1173
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Qy 1021 TGTACAGCATGCTCTTCTGGCTGCAATGTTCAATTCGTTTGTAACTCTTCTGTATC 1080  
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Qy 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTGA 1176  
Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTTAA 1173

## RESULT 3

US-09-875-076-13  
; Sequence 13, Application US/09875076  
; Patent No. 6869776  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chuen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-875-076-13  
  
Query Match 58.4%; Score 686.6; DB 3; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 1.6e-201; Indels 9; Gaps 2;  
Matches 886; Conservative 0; Mismatches 284;  
  
Qy 1 ATGTGCGAGTCTAACAGTACTTGGCATCTTGGCCACCAGCTGCTCAGGTCCCTTGGCAATTT 60  
Db 1 ATGCCAGATACTAATAGCACAAATTTATCACTAGCACTCGTGTACTTTAGCAATTT 60  
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Db 61 TTTATGTCTCTTAGTAGCTTTTGTCTATAAATGCTAGGAAATGCTTTGGTCAITTTAGCTTTT 120  
Qy 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTTCT 180  
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Qy 181 GACTTCTCTGTGGGTGTTGATTTCCATTCCTCTCTGTACATCCCTCACGTGTTGTTTAACTGG 240  
Db 181 GACTTCTTGTGGGTGTTGATCTCCATCTCCTTGTACATCCCTCACAGCTGTTTCAATGG 240  
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Qy 301 TCTGTCTACAAATTTGTCCTCATTAGTACGATCGATACCACTCAGTTCAGTTCAAATGCTGTG 360  
Db 301 TCTGTATATAACATTTGTCCTCATCAGCTATGATCGATACCTGTCACTCAATGCTGTG 360  
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATGTTGCTCAAAATGGTGGCTGTTTGG 420  
Db 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGCTTGG 420  
Qy 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGGAAAGAACAGC 480  
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## RESULT 4

US-09-891-053-2  
; Sequence 2, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891,053  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JP99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1239  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1239)  
US-09-891-053-2

Query Match 14.7%; Score 172.8; DB 3; Length 1239;  
Best Local Similarity 49.6%; Pred. No. 9.9e-43;  
Matches 562; Conservative 0; Mismatches 557; Indels 15; Gaps 4;  
3 GTCCGAGCTAAACAGTACTGGCATCTTGGCCACAGCTGCTCAGTCCCTTGGCAATTTT 62  
60 GCGCGTGCAGGCGGGCGGGCTTCTCGGCTCGCTGGACCGCTGTCTCGCTGGCT 119  
63 AATGTCCTTATTTGCGCTTTTCTATATAATGGTGGCAATGCTGTGGTCATCTTAGCCTTTGT 122

120 CATGGCGTGTCTCATCGTGGCCACAGTACTGGGCAACGGGCTGGTCAATGCTCGCTTCGT 179  
123 GGTGGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTCTGA 182  
180 GCGGGAATTCGAGCTCCGCCACCCAGAAACAACTTCTTTCTGCTCAACCTCGCCATCTCCA 239  
183 CTTCCTCTGGGGTTTGAATTTCCATTCCTCTGTACATCCCTCAGCTGTGTGTTTAAAC---TG 239  
240 CTTCCTCTGGGGTGGCCCTTCTGCAATCCATTTGACGTACCTATGCTGTGACCGGCGGTG 299  
240 GAAATTTGGAAGTGAATCTGCATGTTTGGCTCATTAATGACTATCTTTTGTGACCCG 299  
300 GACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACTACTGTGTGCTC 359  
300 ATCTGTCTACAATATTGTCTCATTTAGCTACGATACCATCAGCTAGTTTCAATGCTGT 359  
360 CTGGTCTTCAACATCGTACTCATCAGCTATGACCGAATTCCTGTGAGTCACTCGAGCTGT 419  
360 GTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTGCTCAATGCTGGCTGTTT 419  
420 CTCTACAGGGCCAGACGGGGACACGAGACGGGCGCTTCGGAAGATGGCATGGTGTG 479  
420 GATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGA-----TTCTTGGAA 473  
480 GGTGCTGGCTTCTCTGTATGGGCTGCGCATCTCTGAGTTGGGAGTACCTGTCTGTG 539  
474 GAACAGACGAAACAAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCAC 533  
540 CAGTTCCATCCCGAGGGGCACCTGCTATGCTGAGTCTTCTTACAACCTGGTACTTTCTCAT 599  
534 CATTACAATGCTCTTGGAAATTCCTGCTTCTGTGCTCATCTCTGTGGCTTATTTCAATGTACA 593  
600 CAGGCTCCACCTCGAGTTCTTACGCCCTTCTCAGCGTTACCTTCTTCAACCTCAG 659  
594 GATTTACTGGAGCTGTGGAAGCTGAGGCTCTCACTGAGGTGCCCTTAGCCATGCTGAT 653  
660 CATCTACCTGAACATCCAGAGCGCACCGGCTTCCGCTTGTATGGGGCGCTGAGGCTGG 719  
654 CTCCACTACTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGTGGCTGGCAGGAC 713  
720 CCAGAAACCCCAACAGATGCCCGCTCGCCACCTCCAGCTCCCCCAGCTGTGGGG 779  
714 AAGTAATCTGTGATTCGAAGGAATCAGTGCATCTCGTCACTCAGAAAGTCTCTCGAAGAAA 773  
780 CTGCTGGCCAAAAGGCGATGGCGAGGCCATGCCGTTGCACAGCTCTGGCAGCTCCTCAAG 839  
774 GAGCAGCATCTCGTGTCTTAAAGACTCATCATGAACAGCAGTATCACTGCTTCAAGT 833  
840 GGGCACTGAGAGGCCACGCTCACTCA---AAGGGGCTCCAAGCCATCAGCATCTTCAGC 896  
834 GGGTTCTTCTGCGATCGGAAGTGCAGGCTTCGCCAAAGGGAGTACGACAGCTTCT 893  
897 ATCCCTGGAGAGCGCATGAAGATGGTGTCCAGAGCATCAACCCAGCGCTTCGGGCTGT 956  
894 CAGAGCAGGAAGCTAGCCAGAGTCACTGGCCATCTTCTGAGCGCTTTTCCCATTTTCTG 953  
957 GCGGGAAGAAGGTGGCCAGTCTGCTGGCCATCATCGTGAAGCATCTTTGGGCTCTGCTG 1016  
954 GGCTCCATATCTGTCTTCACAATGTCCTTTCAATTACCTTACCCAGAACGGAACGCCCAA 1013  
1017 GCGCGGTACACGCTCTTAATGATCATCCAGCTGTGCTTGCATGGCGCTGTCATCCCCGA 1076  
1014 ATCGGTGTGTACAGCATTCGCTTCTGGCTGCAATGTTTCAATTCGTTTCTTAATCCCTT 1073  
1077 TT---ACTGTGACGAGAGCTCTTCTGGCTTCTGTGGGCCAATCGGCCGCTACACCCGT 1133  
1074 TCTGTACCTCTTGTGTACAGGCGTTTCCAGAAAGGCTTTCTGGAAGATATCTTTG 1127  
1134 CCTTACCCACTGTGCCACTACAGCTTCGCGAGAGCGCTTCAACCAAGCTCCTCTG 1187

RESULT 5

US-09-891-053-5  
; Sequence 5, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891.053  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JP99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 2700  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (351)...(1589)  
; NAME/KEY: misc feature  
; LOCATION: (1)...(2700)  
; OTHER INFORMATION: n = A,T,C or G

US-09-891-053-5  
Query Match 14.78; Score 172.8; DB 3; Length 2700;  
Best Local Similarity 49.66; Pred. No. 1.5e-42;  
Matches 562; Conservative 0; Mismatches 557; Indels 15; Gaps 4;  
QY 3 GTGGAGCTTAACAGTACTGSCATCTTGGCCACAGCTGCTCAGTCCCTTGGCATTTT 62  
DB 410 GGGGCTGACAGGGGGGGGGGGCTTCTGGTGGCTGGACCGCTGCTCGCTGGCT 469  
QY 63 AATGTCTTCAATTTGGCTTTGCTATAATGGTAGGAATGCTGTGCTCATCTTAGCTTTGT 122  
DB 470 CATGGCGCTGCTCATGTGGCCACAGTACTGGGCAACGGCTGTCTATGCTGGCTTGT 529  
QY 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTCTGA 182  
DB 530 GGGGATTCAGGCTCGCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGA 589  
QY 183 CTTCCTCGTGGTGTGATTTCCATTCCTCTGTATACCTCCCTCAGTGTGTTTAAAC--TG 239  
DB 590 CTTCCTCGTGGTGGCTTCTGTATCCCATTTGTATGCTACCTTATGCTGACCGGCGGTG 649  
QY 240 GAATTTTGGAGTGGATCTGCATGTTTGGCTCATTAAGTACTATCTTTTGTGCAACCGC 299  
DB 650 GACCTTCGGCGGGGCTCTGCAAGCTGTGGTGGTGTAGACTACCTACTGTGTGCTC 709  
QY 300 ATCTGTCTCAATATTGCTCTCATTAAGTACGATGATGATGATGATGATGATGATGATG 359  
DB 710 CTGGTCTTCAACATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 769  
QY 360 GTCTTATAGGCTCAACACACTGGCATGATGATGATGATGATGATGATGATGATGATG 419  
DB 770 CTCTACAGGGCCAGCAGGGGGGACGAGACGGGGGCTTTCGGAAGATGGCACTGGGTG 829  
QY 420 GATACCTGGCTTCTTGTGTAATAGCCCGATGATTTCTGGCTTCAGAA-----TCTTGGAA 473  
DB 830 GGTGCTGGCTTCTTGTGTAATAGCCCGATGATTTCTGGCTTCAGAA-----TCTTGGAA 473  
QY 474 GAACAGCAGCAACAAAGGACTGTGAGCCTGGCTTTTGTATACAGAGTGTATCATCTCTAC 533

DB 890 CAGTTCCATCCCGAGGGCCACTGCTATGCTAGTCTTCTACAACTGGTACTTCTCAT 949  
QY 534 CATTTACAAATGCTCTTTGGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGACA 593  
DB 950 CACGGCTCCACCTCGAGTTCTTACGGCTTCTTCAAGCTTCTTCAACCTCAG 1009  
QY 594 GATTTACTGAGCTGTGGAAGCTGAGGCTCTCAGTAGTGTGCTTACAGCTTCTTCAAGT 653  
DB 1010 CATCTACCTGAACATCCAGAGGGCGCACCCGCTTTCGGCTTGTATGGGGGGCTGAGGTGG 1069  
QY 654 CTCACCTACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTTCAGGAC 713  
DB 1070 CCAGAACCCACAGATGCCAGCCCTCGCACCTCTGAGCTCCCCCAGCTGCTGGG 1129  
QY 714 AAGTAATCTTGGATTTGAAGGAATCAGCTGCATCTCTGCTCAGTCACTCAAGAAAGTCTTCAAGAAA 773  
DB 1130 CTGCTGGCCAAAAGGCGATGGCGAGGCGCATGCGCTTGCACAGCTCTTGGCAGCTCTCTCAAG 1189  
QY 774 GAGCAGCATCTGCTGCTTAAAGGACTACATGAACAGCAGTATCACTGCTTCAAGT 833  
DB 1190 GGGCAGCTGAGAGGCCAGCTCACTCA---AAAGGGGCTTCCAGCCATCAGCATCTTCAAG 1246  
QY 834 GGGTTCCTTCTGGCGATCGGAAAGTGCAGCGCTTTCGCAAGGGAGTACGACAGCTTCT 893  
DB 1247 ATCCTTGGAGAGCGCATGAAGTGTGCTCCAGAGCATCACCAGCGCTTCGGCTGTC 1306  
QY 894 CAGAGCAGGAAGCTAGCCAGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTG 953  
DB 1307 GCGGACAGAGGTGGCCAAAGTGGTGGCCATCATGTCAGCATCTTTGGGCTCTGCTG 1366  
QY 954 GGTCTCATCTGCTGTTTCAAAATGCTCTTCACTTACCCAGAGGAAAGCCCAAA 1013  
DB 1367 GGGCGCTTACACGCTCTTAAATGATCATCCAGCTGCTTGGCATGCGCGCTGCTATCCCGA 1426  
QY 1014 ATCGTGTGTACAGCATTCCTTCTGGCTGCAATGCTTCAATTCGTTTGTATTCCTT 1073  
DB 1427 TT---ACTGTGACAGAGCTCTTCTGGCTTCTGTGGCCAACTCGGCGCTCAACCCGT 1483  
QY 1074 TCTGTACCTTGTGTACAGGGCTTTCCAGAAAGGCTTCTGGAAGATACCTTTG 1127  
DB 1484 CCTTACCCACTGTGCCACTACAGCTTCCGACAGCGCTTCCACCAAGCTCTCTG 1537

RESULT 6  
US-09-165-543-6  
; Sequence 6, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley

; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1338 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1335  
; US-09-165-543-6

Query Match 12.2%; Score 143.2; DB 3; Length 1338;  
Best Local Similarity 54.2%; Pred. No. 1.4e-33;  
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;  
  
Qy 3 GTCGGAGTCTAACAGTACTGGCATCTTGGCCACACAGCTGCTCAGGTCCCTTGGCAATTTT 62  
Db |||||  
60 GCGCGCTGCAGGCGGGCGCGCGCTTCTCGGCTGCCCTGGACCGCTGCTCCTGGCTGCGCT 119  
Qy |||||  
63 AATGCTCTTCATTTGCGCTTTCGTATAATGGTAGGCAATGCTGTGTGCTCATCTTAGCCTTTGT 122  
Db |||||  
120 CATGGCGCTGCTCATCTGTGGCCACAGTACTGGGGACGCGTGGTCAATGCTCGCCTTCGT 179  
Qy |||||  
123 GGTGGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTCTCGA 182  
Db |||||  
180 GCGGATTCGAGCGCTCGCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGA 239  
Qy |||||  
183 CTTCTCTCGTGGTTTGATTTTCCATTCCTCTGTATACATCCCTCAGCTGTGTTTAAAC---TG 239  
Db |||||  
240 CTTCTCTCGTGGTGGCTTCTGCAATCCCATTTGTACGTACCCCTATGTGTGCTGACCGCGTTG 299  
Qy |||||  
240 GAATTTTGGAGTGAATCTGCATGTTTTCGCTCATTTACTACTGATCTCTTTTGTGCAACGC 299  
Db |||||  
300 GACCTTCGCGCGGGCGCTCTGCAAGCTGTGGCTGGTGGTAGACTACCTACTGTGTGCTC 359  
Qy |||||  
300 ATCTGTCTCAATAATTTGCTCAFTTAGCTAGCATCGATACCGAGTCAGTTTCAAATGCTGT 359  
Db |||||  
360 CTGGTCTTCAACATCGTACTCATCAGCTATGACCGAATCTGTGCTCACTCGAGCTGT 419  
Qy |||||  
360 GTCTTATAGGGCTCAACACACTGCGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTG 419  
Db |||||  
420 CTCCTACAGGGCCACGACGAGGGGGACACGAGACGGGGCGTTTCGGAAGATGGCACTGGTGTG 479  
Qy |||||  
420 GATACGCTTTCTTTGGTAAATGGCCCGATGATTTCTGCTTTCAGAA---TTCTTGGAA 473  
Db |||||  
480 GGTGCTGGCGCTTCTGCTGTATGGGCTGCCATCTCGAGTTGGAGTACCTGTCTGTGG 539  
Qy |||||  
474 GAACAGCACGAACACAAAGGACTGTGAGCCCTGGCTTTGTTACAGAGTGGTACATCCTCAC 533  
Db |||||  
540 CAGTTCCATCCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACCTGGTACTTTCTCAT 599  
Qy |||||  
534 CATTAACATGCTCTTGGAAATTCCTGCTTCTGTGCTCATCTGTGCTGCTTATTTCAATGTACA 593  
Db |||||  
600 CACGGCTCCACCCCTCGAGTTCTTTCAGCGCCCTTCTCAGCGCTTACCTTCTTCAACCTCAG 659  
Qy |||||  
594 GATTTACTGGAGCGCTGTGGAGCGCTA 619  
Db |||||  
660 CATCTACTGAACATCCAGAGGCGCA 685

RESULT 7  
US-09-891-053-26  
; Sequence 26, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo

; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891,053  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JP99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 1953  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (302)...(1636)  
; US-09-891-053-26

Query Match 12.2%; Score 143.2; DB 3; Length 1953;  
Best Local Similarity 54.2%; Pred. No. 1.7e-33;  
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;  
  
Qy 3 GTCGGAGTCTAACAGTACTGGCATCTTGGCCACACAGCTGCTCAGGTCCCTTGGCAATTTT 62  
Db |||||  
361 GCGCGCTGCAGGCGGGCGCGCGCTTCTCGGCTGCCCTGGACCGCTGCTCCTGGCTGCGCT 420  
Qy |||||  
63 AATGCTCTTCATTTGCGCTTTCGTATAATGGTAGGCAATGCTGTGGTCACTATTAGCCTTTGT 122  
Db |||||  
421 CATGGCGCTGCTCATCTGTGGCCACAGTACTGGGCAACGCGCTGCTCATGCTCGCCTTCGT 480  
Qy |||||  
123 GGTGGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTCTCGA 182  
Db |||||  
481 GCGCGATTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGA 540  
Qy |||||  
183 CTTCTCTCGTGGTTCGATTTCCATTCCTCTGTATACATCCCTCAGGTGTGTTTAAAC---TG 239  
Db |||||  
541 CTTCTCTCGTGGTGGCTTCTGCAATCCCATTTGAGGTACCCCTATGTGTGCTGACCGCGTTG 600  
Qy |||||  
240 GAATTTTGGAGTGAATCTGCATGTTTTCGCTCATTTACTGACTATCTTTTGTGCAACGC 299  
Db |||||  
601 GACCTTCGCGCGGGCGCTCTGCAAGCTGTGGCTGGTGTAGACTTACCTACTGTGTGCTC 660  
Qy |||||  
300 ATCTGTCTCAATAATTTGCTCCTCATTTAGCTAGCATCGATACAGTCAGTTTCAAATGCTGT 359  
Db |||||  
661 CTGGTCTTCAACATCGTACTCATCAGCTATGACCGAATCTCTGTGCTCACTCGAGCTGT 720  
Qy |||||  
360 GTCTTATAGGGCTCAACACACTGCGCATCATGAAGATTTGTTGCTCAAAATGGTGGCTGTTG 419  
Db |||||  
721 CTCTACAGGGCCACGACGAGGGGGACGACGAGCGGGCGTTTCGGAAGATGGCACTGGTGTG 780  
Qy |||||  
420 GATACGCTGCTTCTTGGTAAATGGCCCGATGATTTCTGGCTTTCAGA-----TTCTTGGAA 473  
Db |||||  
781 GGTGCTGGCGCTTCTGCTGTATGGGCTGCCATCTGAGTTGGGAGTACCTGTCTGGTGG 840  
Qy |||||  
474 GAACAGCACGAACACAAAGGACTGTGAGCTGGCTTGTGTACAGAGTGGTACATCCTCAC 533  
Db |||||  
841 CAGTTCCATCCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTTCTCAT 900  
Qy |||||  
534 CATTAACATGCTCTTGGAAATTCCTGCTTCTGCTCATCTGTGCTGCTTATTTCAATGTACA 593  
Db |||||  
901 CACGGCTCCACCTCGAGTTCTTTCAGCGCTTCTTCAAGCTTACCTTCTTCAACCTCAG 960  
Qy |||||  
594 GATTTACTGGAGCGCTGTGGAGCGCTA 619

Db 961 CATCTACCTGAACATCCAGAGCGCA 986

US-09-165-543-4  
US-09-165-543-4  
; Sequence 4, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3244 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 778..2112  
; US-09-165-543-4

Query Match 12.2%; Score 143.2; DB 3; Length 3244;  
Best Local Similarity 54.2%; Pred. No. 2.2e-33;  
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

Qy 3 GTCGGAGCTTAACAGTACTGGCATCTTCCACACAGCTGCTCAGTCCCTTGGCATTTT 62  
Db 837 GCGCGCTGACGCGGGCGCGCGCTTCTCGGCTGCTGACCGCTGCTCGCTGCGCT 896

Qy 63 AATGCTCTTCAATTTGCCCTTGTATATAGTAGGCAATGCTGTGCTCATCTTAGCCTTTGT 122  
Db 897 CATGGCGCTGCTCATCTGCGCCACAGTACTGGGCAACGCGTGTGCTCATGCTGCGCTTGT 956

Qy 123 GGTGGACAGAAACCTTAGACATCGAAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182  
Db 957 GCGGATTCGAGCTCGCGCACCCAGAACAACTTTCTGCTCAACCTCGCATCTCCGA 1016

Qy 183 CTTCTCTGCTGGTTTGTATTTCCATCTCTGATACCTCCCTCAGCTGTGTTTAAC---TG 239  
Db 1017 CTTCTCTGCTGGTGGCTTCTGATCTCCCATGCTACGCTATGCTGCTGACCGCGCTGT 1076

Qy 240 GAATTTTGGAGTGAATCTGCATGTTTGTGCTCAATTAAGTATCTTTTGTGACCCG 299  
Db 1077 GACCTTCGCGCGGCGCTCTGCAAGCTGTGGCTGGTGTAGTACTACTGCTGTGCTC 1136

Qy 300 ATCTGTCTACAAATATTGCTCTCATTAGTAGCATCGATCAGTCAATGCTGT 359  
Db 1137 CTGGTCTTCAACATCTGTAATCTCATCAGCTATGAGCGATTCTGTGCTCACTCGAGCTGT 1196

Qy 360 GTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTG 419  
Db 1197 CTCTACAGGGCCAGCAGGGGGACACGAGACGGCGGCTTCGGAGAGATGGCACTGGTGTG 1256

Qy 420 GATACTGGCTTTCTTGTAAATGCGCCGATGATTCTGGCTTCAGA-----TTCTTGGAA 473  
Db 1257 GGTCTGGCTTCTCTGCTGTATGGCCCTGCCATCTGAGTTGGGAGTACCTGTCTGGTGG 1316

Qy 474 GAACAGCAGCAACACAAAGGACTGTGAGCTGTGGCTTTGTTACAGAGTGGTACATCTCAC 533  
Db 1317 CAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTACAACTGGTACTTTCTCAT 1376

Qy 534 CATTACAAATGCTCTTGAATTTCCCTGCTTCTGCTCATCTCTGCTGCTATTTCAATGTACA 593  
Db 1377 CACGGCTCCACCTCGAGTTCTTCAGCGCCCTTCTCAGCGCTTCTCAGCGTTACCTTCTCAACCTCAG 1436

Qy 594 GATTACTGGAGCTGTGGAAGCGTA 619  
Db 1437 CATCTACTGAACATCCAGAGCGCA 1462

RESULT 9  
US-08-985-090-3  
; Sequence 3, Application US/08985090  
; Patent No. 5885893  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl  
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,090  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jean M. Silveri  
; REGISTRATION NUMBER: 39,030  
; REFERENCE/DOCKET NUMBER: MNI-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1335 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1335  
; US-08-985-090-3

Query Match 11.9%; Score 140.4; DB 2; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 1.1e-32;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

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QY 3 GTCGAGTCTAAAGTACTGTCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATTTT 62
DB 60 GCGCGCGCGCGCGCGCGCTTCTCGCAGCCTGGACCGCGGTGCTGGCGCGCT 119
QY 63 AATGCTCTTCAATTTGCTTTGCTAATAAGTGAAGCAATGCTGTGTCATCTTAAAGCTTTTGT 122
DB 120 CATGGCGCTGCTCATCTGCTGGCGCGCTGCTGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCT 179
QY 123 GGTGAGCAGAACTTACATCAGATCAAGTAATTTTCTTAAATTTGGTATTTCTGA 182
DB 180 GCGCGACTCGAGCTTCCGACCCAGAACACTTCTTCTGCTCAACCTCGCATCTCCGA 239
QY 183 CTTCTCTGCTGGGTTTGAATTTCCATCTCTCTGTACATCCCTCACGCTGTTG---TTTAACTG 239
DB 240 CTTCTCTGCTGGCGCGCTTCTGCATCCCACTGTATGTACCTACGCTGCTGACAGCGCGCTG 299
QY 240 GAATTTTGGAGTGAATCTGCATCTGTTTGGCTCAATTAAGTCAATCTTTTGGTGGACCGC 299
DB 300 GACCTTCGGCGCGCGCTCTGCAAGCTGTGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 359
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DB 360 CTTCTGCTTCAACATCTGCTGCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCT 419
QY 360 GTCCTTATAGGCTCAACACACTGTCATCATCAAGATTTGCTCAAAATGGTGGCTGTTTG 419
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QY 420 GATCTGCTTTCTTGGTAAATCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
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QY 474 GAAACAGCAGAACAAAGGACTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
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QY 534 CATTAACATGCTTTGGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
DB 600 CACGGCTTCCACCTGGAGTTCTTACGCGCTTCTCAGCGCTTCTCAGCGCTTCTTAACTCTCAG 659
QY 594 GATTTACTGGAGCTGTGGAAGCTGAGGCTCTCAG 629
DB 660 CATCTACTGAACATCCAGAGCGCGCACCCGCGCTCCG 695
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## RESULT 10

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US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckesman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
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; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-165-543-3
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Query Match 11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 1.1e-32;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCGAGTCTAAAGTACTGTCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATTTT 62
DB 60 GCGCGCGCGCGCGCGCGCTTCTCGCAGCCTGGACCGCGGTGCTGGCGCGCT 119
QY 63 AATGCTCTTCAATTTGCTTTGCTAATAAGTGAAGCAATGCTGTGTCATCTTAAAGCTTTTGT 122
DB 120 CATGGCGCTGCTCATCTGCTGGCGCGCTGCTGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCT 179
QY 123 GGTGAGCAGAACTTACATCAGATCAAGTAATTTTCTTAAATTTGGTATTTCTGA 182
DB 180 GCGCGACTCGAGCTTCCGACCCAGAACACTTCTTCTGCTCAACCTCGCATCTCCGA 239
QY 183 CTTCTCTGCTGGGTTTGAATTTCCATTTCTGTGTAATCCCTCACGCTGTTG---TTTAACTG 239
DB 240 CTTCTCTGCTGGCGCGCTTCTGCATCCCACTGTATGTACCTACGCTGCTGCTGCTGCTGCTGCT 299
QY 240 GAATTTTGGAGTGAATCTGCATCTGTTTGGCTCAATTAAGTCAATCTTTTGGTGGACCGC 299
DB 300 GACCTTCGGCGCGCGCTCTGCAAGCTGTGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 359
QY 300 ATCTGCTACAAATTTGCTCTCATCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 359
DB 360 CTTCTGCTTCAACATCTGCTGCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCT 419
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DB 420 CTCATACCGGCGCGCGCTGACAGCGCGCGCTGACAGCGCGCGCTGACAGCGCGCTGACAGCGCGCT 479
QY 420 GATCTGCTTTCTTGGTAAATCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
DB 480 GGTGCTGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
QY 474 GAAACAGCAGAACAAAGGACTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
DB 540 CAGCTTCACTCCCGAGGCGCACTGCTATGCGCGAGTTCTTCTACAACTGGTACTTCTCTCAT 599
QY 534 CATTAACATGCTTTGGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
DB 600 CACGGCTTCCACCTGGAGTTCTTACGCGCTTCTCAGCGCTTCTCAGCGCTTCTTAACTCTCAG 659
QY 594 GATTTACTGGAGCTGTGGAAGCTGAGGCTCTCAG 629
DB 660 CATCTACTGAACATCCAGAGCGCGCACCCGCGCTCCG 695
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## RESULT 11

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US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
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; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/167,354A  
; CURRENT FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:CDNA  
US-09-167-354-6

Query Match 11.9%; Score 140.4; DB 3; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 1.1e-32;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCGGAGCTAAACAGTACTGGCATCTTGCACACAGCTGCTCAGGTCCCCTTGGCAATTTT 62  
Db 60 GCGCGCGCGCGCGCGCGCGCTTCTCGGCAGCCTGGACCGGTGCTGGCGCGCT 119  
Qy 63 AATGCTCTCAATTTGCCCTTTGCTATAATGTTAGGCAATGCTGTGTCATCTTAGCGCTTTGT 122  
Db 120 CATGGCGCTGCTCATGTCGGCCACGGTGTGGGCAACGGCTGTCACTGCGCTTCGT 179  
Qy 123 GGTGGACAGAAACCTTACATGCAATGTAATATTTTCTTAATTTGGCTATTCTCGA 182  
Db 180 GCGCGACTCGAGCTCGCGACCCAGAACAACTTCTTCTGCTCAACTCGCATCTCCGA 239  
Qy 183 CTTCCTCGTGGTGTGATTTCCATTCCTCTGTATACATCCCTCACGTGTG---TTTAACTG 239  
Db 240 CTTCCTCGTGGCGCTTCTGCATCCCACTGTATGTACCTGTACCTGTGACAGCGCGTG 299  
Qy 240 GAATTTTGGAGTGGAACTCTGCATCTTATTTGGCTCAATTAAGTGTGCTGTTG 299  
Db 300 GACCTTCGGCGCGCGCTCTGCAAGCTGTGGTGTAGTGGACTACCTGTGTGCACTC 359  
Qy 300 ATCTGCTCAATAATTTGCTCTTAATGCTAGTACGATACAGTCAAGTTCATAAATGCTGT 359  
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Db 540 CAGCTCCATCCCAGGGCCACTGCTATGCGAGTCTTCTACAACTGGTACTTCCCTCAT 599  
Qy 534 CATTTACATGCTCTTGGAAATTCCTGCTTCTGTGCTCATCTCTGTGGCTTATTTCAATGTACA 593  
Db 600 CACGGCTTCACCCCTGGAGTCTTTACGCGCTTCTCAGCGTCACTTCTTTAACTCAG 659  
Qy 594 GATTTACTGGAGCTGTGGAGCGTAGGGCTCTCAG 629  
Db 660 CATCTACTGAACTCCAGAGGCGCACCCGCGCTCCG 695

RESULT 12  
US-09-642-855-6  
; Sequence 6, Application US/09642855  
; Patent No. 6413743  
; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/642,855  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:CDNA  
US-09-642-855-6

Query Match 11.9%; Score 140.4; DB 3; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 1.1e-32;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCGGAGCTAAACAGTACTGGCATCTTGCACACAGCTGCTCAGGTCCCCTTGGCAATTTT 62  
Db 60 GCGCGCGCGCGCGCGCGCGCTTCTCGGCAGCCTGGACCGGTGCTGGCGCGCT 119  
Qy 63 AATGCTCTCAATTTGCCCTTTGCTATAATGTTAGGCAATGCTGTGTCATCTTAGCGCTTTGT 122  
Db 120 CATGGCGCTGCTCATGTCGGCCACGGTGTGGGCAACGGCTGTCACTGCGCTTCGT 179  
Qy 123 GGTGGACAGAAACCTTACATGCAATGTAATATTTTCTTAATTTGGCTATTCTCGA 182  
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Qy 183 CTTCCTCGTGGTGTGATTTCCATTCCTCTGTATACATCCCTCACGTGTG---TTTAACTG 239  
Db 240 CTTCCTCGTGGCGCTTCTGCATCCCACTGTATGTACCTGTACCTGTGACAGCGCGTG 299  
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Qy 420 GATACTGGCTTTCTTGGTAAATGGCCGATGATTCGGCTTCAGAT-----TCTTGGAA 473  
Db 480 GGTGCTGGCTTCTCTGTGTACGACAGCACTCTGAGCTGGAGTACCTGTCCGCGGG 539  
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Db 540 CAGCTCCATCCCAGGGCCACTGCTATGCGAGTCTTCTACAACTGGTACTTCCCTCAT 599  
Qy 534 CATTTACATGCTCTTGGAAATTCCTGCTTCTGTGCTCATCTCTGTGGCTTATTTCAATGTACA 593  
Db 600 CACGGCTTCACCCCTGGAGTCTTTACGCGCTTCTCAGCGTCACTTCTTTAACTCAG 659  
Qy 594 GATTTACTGGAGCTGTGGAGCGTAGGGCTCTCAG 629  
Db 660 CATCTACTGAACTCCAGAGGCGCACCCGCGCTCCG 695

RESULT 13  
US-09-642-514-6  
; Sequence 6, Application US/09642514

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; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
; US-09-642-514-6

Query Match      11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 1.1e-32;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCCGAGCTTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGTCCCTTGGCAATTTT 62
Db 60 GCGCGCGCGGGCGCGCGCGCTTCTCGGACGCTGGACCGCGGTGCTGGCGCGCT 119
Qy 63 AATGCTCTTCAATTTGCCCTTGGCTATAATGTTAGGCAATGCTGTGTCATCTTAGCTTTGT 122
Db 120 CATGGCGCTGCTCATCTGTGGCCACGGTGTGGGCAACGGCTGTCATCTCGCTTCGT 179
Qy 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTCGA 182
Db 180 GGCGGACTCGAGCTCGCGCACCCAGAACAACTTCTCTGCTCAACCTCGCATCTCCGA 239
Qy 183 CTTCCTGTGGGTTGATTTCCATTCCTCTGTGATCATCCCTCACGTTG---TTTAACTG 239
Db 240 CTTCCTGTGGCGGCTTCTGATCCCACTGATGTATGATACCTTACCTGTGACAGCGCGCTG 299
Qy 240 GAATTTTGGAGTGGAATCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGCACCGC 299
Db 300 GACCTTGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTACCTGTGTGCACCTC 359
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Db 360 CTCTGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTGCGTCAACCCGAGCGGT 419
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Db 420 CTCATACCGGGCCAGCAGGGTGACACCGCGGGGAGTGGCGAAGATGCTGTGGTGTG 479
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Db 540 CAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTCTACAACTGGTACTTCTCAT 599
Qy 534 CATTAATAGTCTTTGGAATTCCTGCTTCTGTGTCATCTCTGTGGCTATTCTCAATGTACA 593
Db 600 CACGGCTTCCACCTGGAGTTCTTTAGCGCCCTTCTCAGCGCTTCTCAGCGTCACTTCTTAACTCTCAG 659
Qy 594 GATTTACTGGAGCTGTGGAAGCGTAGGGCTCTCAG 629
Db 660 CATCTACTGAACATCCAGAGGGCGCACCCGCTCCG 695
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US-09-642-852-6
; Sequence 6, Application US/09642852
; Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JWJ
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
; US-09-642-852-6

Query Match      11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 1.1e-32;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCCGAGCTTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGTCCCTTGGCAATTTT 62
Db 60 GCGCGCGCGGGCGCGCGCGCTTCTCGGACGCTGGACCGCGGTGCTGGCGCGCT 119
Qy 63 AATGCTCTTCAATTTGCCCTTGGCTATAATGTTAGGCAATGCTGTGTCATCTTAGCTTTGT 122
Db 120 CATGGCGCTGCTCATCTGTGGCCACGGTGTGGGCAACGGCTGTCATCTCGCTTCGT 179
Qy 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTCGA 182
Db 180 GGCGGACTCGAGCTCGCGCACCCAGAACAACTTCTCTGCTCAACCTCGCATCTCCGA 239
Qy 183 CTTCCTGTGGGTTGATTTCCATTCCTCTGTGATCATCCCTCACGTTG---TTTAACTG 239
Db 240 CTTCCTGTGGCGGCTTCTGATCCCACTGATGTATGATACCTTACCTGTGACAGCGCGCTG 299
Qy 240 GAATTTTGGAGTGGAATCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGCACCGC 299
Db 300 GACCTTGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTACCTGTGTGCACCTC 359
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Qy 534 CATTAATAGTCTTTGGAATTCCTGCTTCTGTGTCATCTCTGTGGCTATTCTCAATGTACA 593
Db 600 CACGGCTTCCACCTGGAGTTCTTTAGCGCCCTTCTCAGCGCTTCTCAGCGTCACTTCTTAACTCTCAG 659
Qy 594 GATTTACTGGAGCTGTGGAAGCGTAGGGCTCTCAG 629
Db 660 CATCTACTGAACATCCAGAGGGCGCACCCGCTCCG 695
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RESULT 15

US-09-891-053-21  
; Sequence 21, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891,053  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JF99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JF98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 2050  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (271)...(1629)  
US-09-891-053-21

Query Match 11.9%; Score 140.4; DB 3; Length 2050;  
Best Local Similarity 53.6%; Pred. No. 1.3e-32;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
  
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DB 330 GGCGGGGGGGGGGGGGGGGGCTTCTGGGAGCTGGACCGGGTGGCGCGCT 389  
  
QY 63 AATGTCTTCAATTTGCCCTTGTCTATAATGGTAGGCAATGCTGTGGTCACTTTAGCCTTTGT 122  
DB 390 CATGGCGCTGCTCATCGTGGCCACGGTGTGGGCAACGGCTGCTCATGCTCGCCTTCTGT 449  
  
QY 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTGA 182  
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QY 183 CTTCTCTGTTGGTTTGGATTTCCATCTCTGTACATCCCTCAGCTGTG---TTTAACTG 239  
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QY 240 GAATTTTGGAGTGGAACTCTGCATGTTTGGCTCATTAAGTCACTATCTTTTGTGCAACCGC 299  
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QY 300 ATCTGTCTCAATATTTGCTCTATTAGTACGATCGATCGATCGATTTCAAAATGCTGT 359  
DB 630 CTCTGCTCTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTGCGGTACCCGAGCGGT 689  
  
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DB 690 CTCATACCGGGGCCAGAGGGTGACACCGCGGGGAGTGGGAAAGATGCTGTGGTGTG 749  
  
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DB 750 GGTGCTGGCTTTCTGTGTAATGGCCGATGATTCTGGCTTCAGAT-----TCTTGGAA 473  
  
QY 474 GAACAGACGAAACAAAGAGCTGTGAGCCTTGTGTTTACAGATGGTACATCTCTCAC 533

Db 810 CAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTCTACAACTGGTACTTCCTCAT 869  
QY 534 CATTACAAATGCTCTTTGGAATTCCTGCTTCTCTGTCATCTCTGTGGCTTATTTCATGTACA 593  
DB 870 CAGGGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCTCAGGCTCACCTTCTTTAACCTCAG 929  
QY 594 GATTTACTGGAGCTGTGGAAGCGTAGGGCTCTCAG 629  
DB 930 CATCTACCTGAACATCCAGAGGGCGCACCCGCTCCG 965

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

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Title: US-10-626-445-5

Perfect score: 1176

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Maximum DB seq length: 2000000000

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Maximum Match 100%

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8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
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10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
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12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10J\_PUBCOMB.seq.\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10K\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1176	100.0	1176	9	US-10-626-445-5
2	1176	100.0	1176	10	US-10-626-126-5
3	1176	100.0	1176	10	US-10-626-398-5
4	958.4	81.5	1176	9	US-10-626-445-6
5	958.4	81.5	1176	10	US-10-626-126-6
6	958.4	81.5	1176	10	US-10-626-398-6
7	686.6	58.4	1173	3	US-09-812-216-1
8	686.6	58.4	1173	3	US-09-910-411-1
9	686.6	58.4	1173	3	US-09-875-076-13
10	686.6	58.4	1173	3	US-09-876-252-13
11	686.6	58.4	1173	6	US-10-052-193-1
12	686.6	58.4	1173	7	US-10-272-983-13
13	686.6	58.4	1173	7	US-10-354-769-1
14	686.6	58.4	1173	7	US-10-393-807-13
15	686.6	58.4	1173	7	US-10-417-820A-13
16	686.6	58.4	1173	8	US-10-349-253A-1
17	686.6	58.4	1173	8	US-10-723-955-13

#### ALIGNMENTS

##### RESULT 1

US-10-626-445-5  
; Sequence 5, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-626-445-5

Query Match 100.0%; Score 1176; DB 9; Length 1176;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATCTCGAGGCTTAACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCTCGGCAATTT 60  
Db 1 ATCTCGAGGCTTAACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCTCGGCAATTT 60  
QY 61 TTAATGCTTCATTTGCCITTTGCTATAATGTTAGGCAATGCTGTGTCATCTTAGCCTTT 120  
Db 61 TTAATGCTTCATTTGCCITTTGCTATAATGTTAGGCAATGCTGTGTCATCTTAGCCTTT 120  
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTC 180  
Db 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTC 180  
QY 181 GACTTCTCGTGGTTTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG 240

Sequence 13, Appli  
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Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli



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QY 781 ATCTGTGTCTTAAAGACTCATATGAAACAGACAGTATCATCTGCTTCAAAGTGGGTTC 840
DB 781 ATCTGTGTCTTAAAGACTCATATGAAACAGACAGTATCATCTGCTTCAAAGTGGGTTC 840
QY 841 TTCTGGCGATCGAAAGTGCAGGCTTTCGCAAGAGGAGTACGACAGCTTCTCAGAGGC 900
DB 841 TTCTGGCGATCGAAAGTGCAGGCTTTCGCAAGAGGAGTACGACAGCTTCTCAGAGGC 900
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
DB 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
QY 961 TACTGTCTGTTCACAAATGTCCTTTCAACTTACCCAGAGCGAAGCCCAATCGGTG 1020
DB 961 TACTGTCTGTTCACAAATGTCCTTTCAACTTACCCAGAGCGAAGCCCAATCGGTG 1020
QY 1021 TGGTACAGCAATGCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
DB 1021 TGGTACAGCAATGCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
QY 1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGTACTTTGTGTGACAAAGCAA 1140
DB 1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGTACTTTGTGTGACAAAGCAA 1140
QY 1141 CCAGCGCTGTCCAGAACCAAGTCAATCTCTTTGA 1176
DB 1141 CCAGCGCTGTCCAGAACCAAGTCAATCTCTTTGA 1176
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## RESULT 3

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US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5
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Query Match 100.0%; Score 1176; DB 10; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCCTTGGCATTT 60
DB 1 ATGTGGAGTCTAACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCCTTGGCATTT 60
QY 61 TTAATGTCTTCATTTGCTTGTGCTTATAATGGTAGGCAATGCTGTGTCATCTTTAGCCTTT 120
DB 61 TTAATGTCTTCATTTGCTTGTGCTTATAATGGTAGGCAATGCTGTGTCATCTTTAGCCTTT 120
QY 121 GTGGTGGACAGAACCTTAGACATCGAAGTAAATATTTTCTTAATTTGGCTATTTCT 180
DB 121 GTGGTGGACAGAACCTTAGACATCGAAGTAAATATTTTCTTAATTTGGCTATTTCT 180
QY 181 GACTTCTCTGTGGGTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240
DB 181 GACTTCTCTGTGGGTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240
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## RESULT 4

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US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
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QY 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300
DB 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300
QY 301 TCTGTCTACAAATATGTCCTCATTTAGCTACGATCAGTACAGTTCAGTTCATAATGCTGTG 360
DB 301 TCTGTCTACAAATATGTCCTCATTTAGCTACGATCAGTACAGTTCAGTTCATAATGCTGTG 360
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTTG 420
DB 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTTG 420
QY 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTCTGGCTTTCAGATTCCTTGGAAAGCAGC 480
DB 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTCTGGCTTTCAGATTCCTTGGAAAGCAGC 480
QY 481 ACGAACACAAAGGACTGTGAGCCCTGGCTTTGTTTACAGAGTGGTACATCCTCACCATTACA 540
DB 481 ACGAACACAAAGGACTGTGAGCCCTGGCTTTGTTTACAGAGTGGTACATCCTCACCATTACA 540
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DB 541 ATGCTCTTGGAAATTCCTGCTTCTGTGCTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600
QY 601 TGGAGCTGTGGAAGCGTAGGCTCTCAGTAGTGGCTTACAGAGCTGGGCTTGCAGCAAGAATAA 660
DB 601 TGGAGCTGTGGAAGCGTAGGCTCTCAGTAGTGGCTTACAGAGCTGGGCTTGCAGCAAGAATAA 660
QY 661 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGCTTGCAGCAAGAATAA 720
DB 661 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGCTTGCAGCAAGAATAA 720
QY 721 CCTGGAATGAAGGAATCAGCTGCAATCTGTCATCTCAGAAAAGTCTCAGAAAAGAGCAGC 780
DB 721 CCTGGAATGAAGGAATCAGCTGCAATCTGTCATCTCAGAAAAGTCTCAGAAAAGAGCAGC 780
QY 781 ATCTGTGTCTTAAAGACTCATGAAACAGAGTATCATCTGCTTCAAAGTGGGTTC 840
DB 781 ATCTGTGTCTTAAAGACTCATGAAACAGAGTATCATCTGCTTCAAAGTGGGTTC 840
QY 841 TTCTGGCGATCGAAAGTGCAGGCTTTCGCAAGAGGAGTACGACAGCTTCTCAGAGGC 900
DB 841 TTCTGGCGATCGAAAGTGCAGGCTTTCGCAAGAGGAGTACGACAGCTTCTCAGAGGC 900
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
DB 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
QY 961 TACTGTCTGTTCACAAATGTCCTTTCAACTTACCCAGAGCGAAGCCCAATCGGTG 1020
DB 961 TACTGTCTGTTCACAAATGTCCTTTCAACTTACCCAGAGCGAAGCCCAATCGGTG 1020
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DB 1021 TGGTACAGCAATGCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
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QY 1141 CCAGCGCTGTCCAGAACCAAGTCAATCTCTTTGA 1176
DB 1141 CCAGCGCTGTCCAGAACCAAGTCAATCTCTTTGA 1176
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; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Query Match      81.5%; Score 958.4; DB 9; Length 1176;
Best Local Similarity 88.4%; Pred. No. 7.4e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATT 60
DB 1 ATGTCGGAGTCTAACGGCACTGACGCTTGCCACTGACTGCTCAAGTCCCTTGGCAATT 60
QY 61 TTAATGTCTTCAATTGCTTTGTCTATAAATGGTAGGCAATGCTGTGTCATCTTTAGCCTTT 120
DB 61 TTAATGTCCCTGCTTGTCTTTGTCTATAAAGATAGGCAATGCTGTGTCATCTTTAGCCTTT 120
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DB 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
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QY 241 AATTTTGGAAAGTGGAAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300
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DB 301 TCCGCTCTACAGTATTTGCTCTCATTTAGTAGATCGATACAGTCAGTCAGTTTCAAAATGCTGTG 360
QY 361 TCTTATAGGCTCAACACACTGTCATCATGAAGATTTGCTCAAAATGTTGGCTGTTTGG 420
DB 361 CGTTATAGACACAGACACTGGCATCTGCAATTTGTTGCTCAAAATGTTGGCTGTTTGG 420
QY 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGGAAAGAACAGC 480
DB 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGGAAAGAACAGC 480
QY 481 ACGAACACAAAGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA 540
DB 481 ACCAACACACAGAGAGTGCAGGCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540
QY 541 ATGCTCTTGGAAATCTGCTGCTCATCTCTGCTGCTTATTTTCAATGACAGATTTTAC 600
DB 541 GCATTCCTTGGAAATCTGCTGCTCATCTCTGCTGCTTATTTTCAATGACAGATTTTAC 600
QY 601 TGGAGCCTGTGGAAAGCTGAGGCTCTCAGTAGGTGCTCAGTACGCTAGCCATGCTGATTTCTCCACT 660
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DB 661 ACCTTCTCAGGAGGCACTGAGACACTCAGCAGAACTGGGTGGCTTGTAGGACAAAGTCTT 720
QY 721 CCTGGATTGAAGAAATCAGCTGATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780
DB 721 CCTGGATTGAAGAAACAGCCCGCATCCCTCATTCAGAAAGTCCAGAGAAAGAGCAGT 780
QY 781 ATCCTGGTGTCTTAAAGACTTCATGAAACAGCAGATATCATCTGCCCTCAAAGTGGGTTC 840
DB 781 ATCCTGGTGTCTTAAAGACTTCATGAAACAGCAGATATCATCTGCCCTCAAAGTGGGTTC 840
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DB 781 CTCTGGTGTCTTAAAGACTCACATGAGGGTAGTATCATCGCCTTCAAAGTGGGTTC 840
QY 841 TTCTGGCGATCGAAAGTGCAGGCTTCGCCAAAGGGAGTACGACAGCTTCTCAGAGGC 900
DB 841 TTCTGGCGATCAGAAAGCCAGTGTCTTCCAGAGAGAGACCTGGAGCTTCTCAGAGGC 900
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTTGAGCGCTTTTGGCCATTTGCTGGGTCCA 960
DB 901 AGGAAGCTAGCCAGGTCTAGTGTCTCTGAGTGTCTTGGCCATTTGCTGGGTCCG 960
QY 961 TACTGTCTGTTCACAAATGTCCTTCAACTTACCCAGAACGGACGCCCAATCGGTG 1020
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QY 1021 TGTACAGCATTTGCCCTTCTGGCTGCAATGTTCAATTTGTTTCTTAATCCCTTCTGTAC 1080
DB 1021 TGTACAGCATGACCTTTTGGCTACAGTGTTCNAATCTTAATCCCTTCTATAC 1080
QY 1081 CCTTTGTGCACAGGCGTTTCCAGAAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140
DB 1081 CCTTTGTGCACAGAGCTTTCCAGAAAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA 1140
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DB 1141 CCAGCACCTTTCACAGACCCAGTCAGTATCTTCTTGA 1176

RESULT 5
US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Chongli
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Query Match      81.5%; Score 958.4; DB 10; Length 1176;
Best Local Similarity 88.4%; Pred. No. 7.4e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATT 60
DB 1 ATGTCGGAGTCTAACGGCACTGACGCTTGCCACTGACTGCTCAAGTCCCTTGGCAATT 60
QY 61 TTAATGTCTTCAATTGCTTTGTCTATAAATGGTAGGCAATGCTGTGTCATCTTTAGCCTTT 120
DB 61 TTAATGTCCCTGCTTGTCTTTGTCTATAAAGATAGGCAATGCTGTGTCATCTTTAGCCTTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
DB 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
QY 181 GACTTCCTCGTGGTGTGATTTCCATTCCTCTGATCATCCCTCACGCTGTTTAACTGG 240
DB 181 GACTTCCTCGTGGTGTGATCTCCATTCCTCTGATCATCCCTCACGCTGTTTAACTGG 240
QY 241 AATTTTGGAAAGTGGAAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300
DB 241 AATTTTGGAAAGTGGAAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
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QY 301 TCTGTCTACAAATATGTCCTCATTAGCTACGATCGATACCACTCAGTTTCAAAATGCTGTG 360
Db 301 TCCGTCTACAGATATGTCCTCATTAGCTACGATCGATACCACTCAGTTTCAAAACGCTGTG 360
QY 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTGCTCAAAATGGTGGCTGTTTGG 420
Db 361 CGTTATAGAGCACACACTGGCATCTGCAATCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGG 420
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTCCTGGCTTCAGATTCTTGGGAAGAACAGC 480
Db 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTCCTGGCTTCGGATTCTTGGGAAGAACAGC 480
QY 481 ACGAACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACA 540
Db 481 ACCAACACAGAGGATGCGAGCTGGCTTTGTTACTGAGTGGTACATCTCCTGCCATTACA 540
QY 541 ATGCTCTTGGAAATTCCTGCTTCCTGTCACTCTGTGGCTTATTTCAATGTACAGATTTAC 600
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QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTACGCCATGCTGGATTCTCCACT 660
Db 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTACGCCATGCTGGATTCTCCACT 660
QY 661 ACCTCTTCAGTGTCTCAGGACACTTACAGAGCTGGGTGGCTTGGCAGGACAAAGTAAT 720
Db 661 ACCTCTTCAGGCGCACTGGACACTCACGCAAGACTGGGTGGCTTGTAGGACAAAGTCTT 720
QY 721 CCTGGATTGAAGGAATCAGCTGCATCTGCTCACTCAGAAAGTCTCCGAAGAAAGCAGC 780
Db 721 CCTGGATTAAAGGAACACGCCGATCCCTCTCATTCAGAAAGTCCACGAGAAAGCAGT 780
QY 781 ATCTGTGTCTTTAAGGACTCACATGAACAGAGTATCACTGCTCTTCAAAAGTGGTTC 840
Db 781 CTCCTGGTGTCTTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGTTC 840
QY 841 TTCTGGCGATCGAAAGTGCAGCGCTTCGCCAAAGGAGTAGCAGAGCTTCTCAGAGC 900
Db 841 TTCTGCCGATCAGAAAGCCAGTGTCTTACCAGAGAGACGCTGGAGCTTCTCAGAGC 900
QY 901 AGGAAGCTAGCAGGCTCACTGGCCATCTCTGAGCGCTTTTGCATTTGCTGGGCTCCA 960
Db 901 AGGAAGCTAGCAGGCTCGTAGCTGTCTCTGAGTGTCTTTGCCATTTGCTGGGCTCCG 960
QY 961 TACTGTCTGTTTCAAAATGTCCTTTCAACTTACCCAGAAACGGAACGCCCAAAATCGGTG 1020
Db 961 TATTGCTGTTTCAAAATGTTCTTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGATT 1020
QY 1021 TGGTACAGCATGCTCTGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080
Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCACCTTAAATCCCTTTCTATAC 1080
QY 1081 CCTTTGTGCAGCGCTTTCCAGAAGCTTTCTGGAAGTACTTTCTGTGACAAAGCAA 1140
Db 1081 CCTTTGTGCCACAGACGTTTCCAGAAGCTTTCTGGAAGTACTTCTGTGACAAAGCAA 1140
QY 1141 CCAGCGCTGTGCAGAACCACTCAGTATCTCTTGA 1176
Db 1141 CCAGCACTTCACAGACCAGTCAATCTCTTGA 1176
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## RESULT 6

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US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
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; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6
```

Query Match 81.5%; Score 958.4; DB 10; Length 1176;

Best Local Similarity 88.4%; Pred. No. 7.4e-291;  
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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QY 1 ATGTCGAGTCTAACAGTACTGGCATCTTGGCACAGCTGTCTCAGGTCCCTTGGCATTT 60
Db 1 ATGTCGAGTCTAACGGCAGCTGACGTCTTGCACCTGACTGCTCAAGTCCCTTGGCATTT 60
QY 61 TTAATGCTTTCATTTGGCTTTGCTTATTAATGGTAGGCAATGCTGTGGTCAATCTTAGCCTTT 120
Db 61 TTAATGCTTTCATTTGGCTTTGCTTATTAACGATAGGCAATGCTGTGGTCAATCTTAGCCTTT 120
QY 121 GTGCTGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
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QY 301 TCTGTCTACAAATATGTCCTCATTAGCTACGATCGATACCACTCAGTTTCAAAATGCTGTG 360
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QY 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTGCTCAAAATGGTGGCTGTTTGG 420
Db 361 CGTTATAGAGCACAGCACACTGGCATCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGG 420
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTCCTGCTTCAGATTCTTGGGAAGAACAGC 480
Db 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCGCTTCGGATTCTTGGGAAGAACAGC 480
QY 481 ACGNACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA 540
Db 481 ACCAACACAGAGGATGCGAGCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540
QY 541 ATGCTCTTGGAAATTCCTGCTTCCTGTCACTCTGCTGGCTTATTTCAATGTACAGATTTAC 600
Db 541 GCATTCCTTGGAAATTCCTGCTTCCTGTCTCTGTTGGTGTCTATTTCAAGTGTACAGATTTAC 600
QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTTAGCCATGCTGGATTCTCCACT 660
Db 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTTAGCCATGCTGGATTCTCCACT 660
QY 661 ACCTCTTCAGTGTCTCAGGACACTTACAGAGCTGGGTGGCTTGGCAGGACAAAGTAAT 720
Db 661 ACCTCTTCAGGCGCACTGGACACTCACGCAAGACTGGGTGGCTTGTAGGACAAAGTCTT 720
QY 721 CCTGGATTGAAGGAATCAGCTGCATCTGCTCACTCAGAAAGTCTCCGAAGAAAGCAGC 780
Db 721 CCTGGATTAAAGGAACCCGCGCATCCCTCTCATTCAGAAAGTCCACGAGAAAGCAGT 780
QY 781 ATCTGTGTCTTTAAGGACTCACATGAACAGAGTATCACTGCTCTTCAAAAGTGGTTC 840
Db 781 CTCCTGTGTCTTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGTTC 840
QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGAGTAGCAGAGCTTCTCAGAGC 900
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841 TTCTGCCGATCAGAAAGCCAGTGTCTTCCACAGAGAGACGCTGGAGCTTCTCAGAGGC 900
901 AGAAGCTACGAGGTCACTGGCCATCTCTCTGAGCGCTTTTGGCCATTTTCTGGGCTCCA 960
901 AGAAGCTACGAGGTCACTGGCTGTCTCTCTGAGTGTCTTTTGGCAATTTTCTGGGCTCG 960
961 TACTGTCTGTTCACAAATTTGCTTTCCTTCAACTTACCCAGAAAGGAAAGCCCAAAATCGGTG 1020
961 TATTGCTGTTCACAAATTTGCTTTCCTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGAAT 1020
1021 TGGTACAGCATAGCTTCTGGCTGCAATTTCAATTTGTTAATCCCTTCTGTATC 1080
1021 TGGTACAGCATAGCTTCTGGCTGCAATTTCAATTTGTTAATCCCTTCTGTATC 1080
1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATCTCTGTGTGACAAAGCAA 1140
1141 CCAGCGTGTACAGAACCACTGATGATCTTCTTGA 1176
1141 CCAGCACTTACAGAACCACTGATGATCTTCTTGA 1176

RESULT 7
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Query Match      58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATTT 60
DB 1 ATGCCAGATCTAATAGACAACTCAATTTATCACTAGACACTCGTGTACTTTAGCAATTT 60
QY 61 TTAATGCTTCATTTGGCTTTGTCTATTAATGGTAGGCAATGCTGTGGTCACTTTAGCCCTTT 120
DB 61 TTTATGTCCTTAGTAGCTTTTGTCTATTAATGCTAGGAAATGCTTTGGTCAATTTTAGCTTTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCT 180
DB 121 GTGGTGACAGAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180
QY 181 GACTTCTCTCGTGGTGTGATTTCCATTTCCCTCTGTACATCCCTCAGCTGTGTTTAACTGG 240
DB 181 GACTTCTTCTGGGTGTGATCTCAATCTCTTTGTACATCCCTCAGCGTGTTCGAATGG 240
QY 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCAATTACTGACTATCTTTTGTGACCGCA 300
DB 241 GAATTTTGGAAAGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
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QY 301 TCTGTCTACAAATATGTCTCTCATTAGCTACGATCGATACAGTCAGTTTCAAAATGCTGTG 360
DB 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTCTCAGTCTCAAAATGCTGTG 360
QY 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTGG 420
DB 361 TCTTATAGAACTCAACATACACTGGGGTCTTGAAGATTGTTTACTCTGTATGGTGGCGGTTTGG 420
QY 421 ATACTGGCTTTCTTGTGTAATGSCCGATGATTTCTGGCTTTCAGATTTCTTGGAAAGAACAGC 480
DB 421 GTCTGCGCTTCTTGTGTAATGSCCGCAATGATTTCTAGTTTTCAGAGTCTTGGAAAGGA --- 476
QY 481 ACGAACACAAAGACTGTGTAGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATACATCTTGGCATCACA 534
QY 541 ATGCTCTTGTGAATTTCTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 600
DB 535 TCATTTCTTGGAAATTCGTGTATCCAGTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 594
QY 601 TGGAGCTGTGGAGCGGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTTCTCCACT 660
DB 595 TGGAGCTGTGGAGCGGTAGTATCTCAGTAGGTGCCAAAGCCATCTCGACTGCTGCT 654
QY 661 ACCTCTTCCAGTGTCTTCCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
DB 655 GTCTCTTCCAACTCTGTGGACACTCATTTCCAGAGGTAGACTATCTTCAAGSAGATCTCTT 714
QY 721 CCTGGATTGAAGGAATCAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 780
DB 715 TCTGCATCGACAGAAAGTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 774
QY 781 ATCTGTGTGCTTAAAGGACTCAGTGAACAGAGTATCACTGCTTCAAAGTGGGTTC 840
DB 775 CTATGTTTCTTCCAAAGACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGGTTC 834
QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTTCGCCAAAGGAGTACGACAGCTTCTCAGAGGC 900
DB 835 TTCTCCCAATCAGATTTCTGTAGTCTTCCAAAGGGAACATGTTGAATCTGTAGAGCC 894
QY 901 AGAAGCTACCGAGTCACTGGCATCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 960
DB 895 AGGAGATTAGCCAAAGTCACTGGCCATTTCTTAGGGGTTTTTGTCTGTCTGTCTGTCTGTCT 954
QY 961 TACTGTCTGTTCACAAATTTGCTTCAACTTACCCAGAGGAGCGCCCAAAATCGGTG 1020
DB 955 TATTCTCTGTTCACAAATTTGCTTCAATTTTATTTCTCAGAACAGGTCTCTTAAATCAGTT 1014
QY 1021 TGGTACAGCATTTGCTTCTGGCTGCAATGGTTCAATTTGTTTGTATCTCCCTTTCTGTATC 1080
DB 1015 TGGTATAGAAATTCGATTTTGGCTTCACTGTGTCAATTTCCCTTGTCAATCTCTTTTGTAT 1074
QY 1081 CCTTTGTGTCAAGCGCTTTCAGAGGCTTTCGGAAGATCTTTGTGTGACAAAGCAA 1140
DB 1075 CCATTTGTGTCAAGCGCTTTCAGAAAGGCTTCTTGGAAATATTTTGTATATAAAAGCAA 1134
QY 1141 CCAGCGTGTGCAGAGAC---CAGTCAATCTTCTTGA 1176
DB 1135 CCTTACCATCACAAACACAGTCGCTCAGTATCTTCTTAA 1173
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RESULT 8
US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
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; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match      58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTGCGCACAGCTGCTCAGGTCCTCGGCAATTT 60
Db 1 ATGCCAGATCTAATAGACAAATCAATTTATCACTAAGCACTGCTGTACTTTAGCAATTT 60
Qy 61 TTAATGCTTCATTTGGCTTTGCTATTAATGCTAGGCAATGCTGTGGTCATCTTAGCCCTTT 120
Db 61 TTTATGCTCTTAGTAGCTTTTGGCTATTAATGCTAGGAAATGCTTTGGTCAATTTTAGCTTTT 120
Qy 121 GTGCGTGACAGAAACCTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTTCT 180
Db 121 GTGCGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTGGCCATCTCT 180
Qy 181 GACTTTCCTCGTGGGTTTGATTTCCATTCCTCTGACATCCCTCACGCTGTTGTTAACTGG 240
Db 181 GACTTCTTTGGGTGTGATCTCAATTCCTTTGTACATCCCTCACAGCTGTTGCAATGG 240
Qy 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCAATTAAGTCAATCTTTTGTGCAACGCCA 300
Db 241 GAATTTGGAAAGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTATGACACA 300
Qy 301 TCTGTCTACATATTTGCTTCATTTAGCTACAGATGATACAGTACAGTTCAAATGCTGTG 360
Db 301 TCTGTATATAACATTTGCTTCATTCAGTATGATGATACATCTGTCAGTCTCAAAATGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACACTACTGGGCTCTTGAGATTTGTTACTCTGATGTTGGCGCTTGG 420
Qy 421 ATACTGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGGAAAGAACGC 480
Db 421 GTGCTGCTCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGGA--- 476
Qy 481 ACGAACACAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTATACCTCCACCATTTACA 540
Db 477 --TGAAGGTAGTGAATGGAACCTGGATTTTTCGGAATGGTATACCTCTTGGCCATCACA 534
Qy 541 ATGCTCTTGGAAATTCCTGCTCTCATCTGCTGCTTATTTCAATGTATACAGATTTAC 600
Db 535 TCATTTCTTGGAAATTCGTAATCCAGTCTATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
Qy 601 TGGAGCTGTGGAAAGCTAGGGCTCTCAGTAGGTGCGCTAGCCATGCTGGATTTCTCCACT 660
Db 595 TGGAGCTGTGGAAAGCTAGTATCTCAGTAGGTGCGCAAGCCATCTGAGACTGACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGTGGCTTCAGAGCAAGATTAAT 720
Db 655 GTCTCTTCCAACTCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714
Qy 721 CCTGGATTGAGGAATCAGCTGCAATCTCGTCACCTCAGAAATGCTCCTCAAGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAAGTTCTTCGTCATCTCTTTCATTCAGAGAGACAGAGGAGAAAGAGTAGT 774
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Qy 781 ATCTGGTGCTCTTAAGGACTCACATGAACAGCAGATATCACTGCTTCAAAGTGGGTTCC 840
Db 775 CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATAACAATTGCTTCCAAAATGGGTCC 834
Qy 841 TTCTGGCGATCGGAAAGTGCAGGCTTCGCGCAAGGAGTACGACAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGCTTCTTCCAAAGGGAACATGTTGAACCTTAGAGCC 894
Qy 901 AGGAAGCTAGCAGGTCACCTGCGGCATCCTTCTGAGCCCTTTTGGCCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCCAAGTCACTGGCCATTTCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy 961 TACTGCTGTTTCAATTTGCTTCAACTTTACCCAGAGACGGAACGCCCAAAATCCGCTG 1020
Db 955 TATTTCTGTGTCAAAATTTGCTTCAATTTATTTCTCAGAACAGAGTCTTAATCAATGTT 1014
Qy 1021 TGTACAGCAATTCCTTCTGGCTGCAATGTTCAATTCGTTTGAATCCCTTTCTGTATC 1080
Db 1015 TGGTATAGAATTCATTTTGGCTTTCAGTGGTTCATTTCCCTTTGTCATCTCTTTTGTAT 1074
Qy 1081 CTTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGTACAGGCGTTTCCAAAGGCTTTCTTGAATAATATTTGTATATAAAAGCAA 1134
Qy 1141 CCAGCGCTGTACAGAC---CAGTCAGTATCTCTTGA 1176
Db 1135 CCTTACCATCAACAACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 9
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
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; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-875-076-13

Query Match      58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGCTCTACAGTACTGGCATCTTGCACACAGCTGCTCAGGTCCTCGGCAATTT 60
Db 1 ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGCTCTTATTTGGCTTTGCTATTAATGGTAGGCAATGCTGTTGTCATCTTAGCCCTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGGCTATTAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120
Qy 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTTTCCTTAATTTGGCTATTTCT 180
Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTTTTCCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCCTCGTGGTGTGATTTTCATTCCTCTGTACATCCCTCACGCTGTTTGAATCGG 240
Db 181 GACTTCCTTGTGGTGTGATTCCTCATCTCCTTTGTACATCCCTCACGCTGTTTGAATCGG 240
Qy 241 AATTTTGAAGTGAATCTGCAATCTGATGTTTGGTCAATTAATGCTATCTTTTGTGACCGCA 300
Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTATGACGCA 300
Qy 301 TCTGTCTACAAATTTGTCCTCATTTAGCTAGCATACGATACAGTCTCAGTTTCAAAATGCTGTG 360
Db 301 TCTGTATATACATTTGCTCATCAGATATGATGATACCTGTCAGTCTCAAAATGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGCTGTGTTGGT 420
Db 361 TCTTATAGAACTCAACACTACTGGGCTCTTGAAGATTTGTTACTCTGTATGTTGGCGT 420
Qy 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480
Db 421 GTGTCGGCTTCTTGTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGAAGGA 476
Qy 481 ACGAACACAAGGACTGTGACCTGGCTTGTGTTACAGAGTGGTACATCTCCACCATTAACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAAATGGTATCCTTGGCCATCACA 534
Qy 541 ATGCTCTTGAATTTCTGCTTCTGTCATCTCTGCTTATTTTCAATGTACAGATTTTAC 600
Db 535 TCATTTCTTGAATTTCTGTCATCTTCTGCTTATTTTCAACATGATATTTAT 594
Qy 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTCCTGACCGATGTCGATTTCTCCACT 660
Db 595 TGGAGCTGTGGAAGCGTAGATCTCAGTAGGTCGCAAAAGCCATCTCGGACTGACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTCAGACACTTACACAGAGCTGGGTGGCTTCAGACAGAGTAAT 720
Db 655 GTCTCTTCCAAACATCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 721 CCTGGATTGAAGGAATCAGCTGTCATCTCGTCACTTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780
Db 721 CCTGGATTGAAGGAATCAGCTGTCATCTCGTCACTTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780
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Db 715 TCTGCAATCGAGAAAGTTCTGTCATCTTTCATTCAGAGAGACAGAGGAGAAAGAGTAGT 774
Qy 781 ATCTGCTGTCTTAAAGACTCACATGAACAGACAGATATCACTGCTTCAAAAGTGGGTTC 840
Db 775 CTCAATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834
Qy 841 TTCTGGCGATCGAAAAGTGCAGCGCTTCGCAAAAGGAGTACGCGAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCAACCAAAAGGAAACATGTTGAATCTGTAGAGCC 894
Qy 901 AGGAAGCTAGCAGGTCACTGGCCATCTTCTCAGCGCTTTTCCCATTTCTGGGCTCCA 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTTCTTCTAGGGGTTTTTCTGCTGTTCTGGGCTCCA 954
Qy 961 TACTGCTGTTCACAATTTGCTCTTCAACTTACCCAGAACGGAACGCCCAAAATCGGTG 1020
Db 955 TATCTCTGTTTCAAAATGTCCTTTCAATTTATTTCTCAGCAACAGGTCTCTAATCAATT 1014
Qy 1021 TGGTACAGCAATTCCTTCTGGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTCTGTATC 1080
Db 1015 TGGTATAGAAATTCGATTTTGGCTTTCAGTGGTTCATTTCTTGTCAATCCTCTTGTAT 1074
Qy 1081 CCTTGTGTCAAGGCTTTCCAGAAAGCTTCTGGAAGATACCTTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGTCAAGGCTTTTCAAAAGGCTTCTTGAATAATATTTGTATATAAAAGCAA 1134
Qy 1141 CCAGCGCTGTCAAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CCTTACCATCACAAACAGTCGCTCAGTATCTTCTTAA 1173

RESULT 10
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled R
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
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Query Match	58.4%;	Score 686.6;	DB 3;	Length 1173;
Best Local Similarity	75.1%;	Pred. No. 4.7e-205;		
Matches 886;	Conservative 0;	Mismatches 284;	Indels 9;	Gaps 2
Qy	1	ATGTCGGAGTCTAACAGTACTGGGCATCTTGGCCACCAGCTGCTCAGTCCCTTGGCATTT	60	
Db	1	ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT	60	
Qy	61	TTAATGTCCTCATTTGGCTTTGCTATATATGGTGGCAATGCTGTGCTCATCTTACGCCCTTT	120	
Db	61	TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCATTTTAGCTTTT	120	
Qy	121	GTGCTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTTCTTAAATTTGGCTATTCT	180	
Db	121	GTGCTGGACAAAACCTTAGACATCGAAGTAGTTATTTTTTCTTAACTGGCCATCTCT	180	
Qy	181	GAC TTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTGTTAACTGG	240	
Db	181	GAC TTCCTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACA CGCTGTTCCGAATGG	240	
Qy	241	AAATTTTGGAGTGGAACTCTGCATGTTTTGGCTCATTACTGTACTATCTTTTGGCACCCCA	300	
Db	241	GATTTTGGAAAGSAAATCTGTGATTTTTGGGTCACTACTGACTATCTGTATTATGTACAGCA	300	
Qy	301	TCCTGCTCAAAATATTTGTCCTCATTTAGCTACGATCGATACCACTCAGTTGTTCAAATGCTGTG	360	
Db	301	TCCTGATATAACATTTGTCCTCATCAGCTATGATCGATACCTGTCACTTCAAATGCTGTG	360	
Qy	361	TCCTTATAGGGCTCAACACACTGGGCATCATGAAGATTGTTGCTCAAATGGTGCTGTTTGG	420	

US-10-052-193-1

Query Match 58.4%; Score 686.6; DB 6; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 4.7e-205;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGCTAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCTTGGCAATTT 60  
DB 1 ATGCCAGATATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

QY 61 TTAATGTCCTTCAATTTGGCTTTGCTATAATGGTAGGCAATGCTGGTGCATCTTAGCCCTTT 120  
DB 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120

QY 121 GTGGTGACAGAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
DB 121 GTGGTGACAGAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCAATCTCT 180

QY 181 GACTTCTCTGGGTTTGATTTCCATTTCTCTGTACATCCCTCACGCTGTTTAACTGG 240  
DB 181 GACTTCTTTGGGTGTGATCTCAATTCCTTTGTACATCCCTCACAGCTGTTTGAATGG 240

QY 241 AATTTTGGAGTGAATCTGCAATTTGGCTGCTATTAAGTCACTATCTTTTGTGACCGCA 300  
DB 241 GATTTTGGAAAGGAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300

QY 301 TCTGTCTACAAATTTGTCCTCATTTAGCTAGCATGATCAGTACACAGTCAGTTTCAAAATGCTGTG 360  
DB 301 TCTGTATATAACATTTGTCCTCATCAGCTATGATGATGATCTGTCAGTCTCAAAATGCTGTG 360

QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTCCTCAAAATGCTGGCTTTTGG 420  
DB 361 TCTTATAGAACTCAACACTGCGGTCTTGAAGTTGTTACTCTGAAGTGGCGCTTTGG 420

QY 421 ATACTGCTTTCTTGGTAAATGGCCCGATGATTCCTGGCTTCAGATTTCTTGAAGAAACAGC 480  
DB 421 GTGCTGGCTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGAAGGA---- 476

QY 481 ACGAACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCCACCAATACA 540  
DB 477 --TGAAGTGTAGTGAATGTAACCTGGATTTTTCGGAATGGTACATCTCTGGCATCACA 534

QY 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600  
DB 535 TCATTTCTGGAATTCGTGATCCCGATCATCTTAGTCTGCTTATTTCAACATGAATTTAT 594

QY 601 TGGAGCTCTGGAAGCGTAGGCTCTCAGTAGTGGCCCTAGCCATGCTGGAATCTCCACT 660  
DB 595 TGGAGCTGTGGAAGCGTGTATCTCAGTAGTGGTCCAAAGCCATCTGGACTGACTGCT 654

QY 661 ACCTTCTCAGTCTTACAGACATTTACAGAGCTGGGTGGCTTCCAGGACAAAGTAAT 720  
DB 655 GTCTCTTCCAAACATCTGTGACATCTCAATCAGAGGTAGATATCTTCAAGAGATCTCTT 714

QY 721 CCTGGAATGAAGGAATCAGCTGCAATCTCGTCACTCAGAAAGTCTCTCGAAAGAGCAGC 780  
DB 715 TCTGCACTCAGAGAGTCTCTGCACTCTTCACTTACAGAGACAGAGAGAGAGTAGT 774

QY 781 ATCTGTGTCTTAAAGACTCAATGAACAGCAGTATCACTGCTTCAAGTGGGTTC 840  
DB 775 CTCATGTTTCTCCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834

QY 841 TCTGGCGATCGGAAGTGAAGCGCTTCCGCAAGAGGAGTACGAGAGCTTCTCAGAGGC 900  
DB 835 TTCTCCCAATCAGATCTCTGAGTCTTCCCAAGAGGGAACATGTTGAATGCTTAGAGCC 894

QY 901 AGGAAGCTAGCCAGTCACTGGCCATCTCTCTGAGCGCTTTGCAATTTGCTGGGCTCCA 960  
DB 895 AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTGTGTTGCTGGGCTCCA 954

QY 961 TACTGTCTGTTTCAAAATTTGCTTTCAACTTTACCCAGAAACCGGAAACCCCAAAATCGGTG 1020  
DB 955 TATTTCTGTTTCAAAATTTGCTTTTCAATTTATTTCTCAGCAACAGGTCCTTAAATCAGTT 1014

QY 1021 TGGTACAGCATTCCTTCTGGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080  
DB 1015 TGGTATAGAATTCGCAATTTGGCTTCAGTGCTTCAATTCCTTTCTCAATCCTCTTTGTAT 1074

QY 1081 CTTTGTGTACAGGCGTTTCCAGAAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140  
DB 1075 CCATTTGTGTACAGGCGTTTCCAAAGGCTTTCTTGAATAATATTTGTATATAAAAGCAA 1134

QY 1141 CAGCCCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176  
DB 1135 CCTCTACCATCAACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 12

US-10-272-983-13  
; Sequence 13, Application US/10272983  
; Publication No. US20030148450A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/272,983  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-272-983-13

Query Match 58.4%; Score 686.6; DB 7; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 4.7e-205;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGCTAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCTTGGCAATTT 60  
DB 1 ATGCCAGATATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

QY 61 TTAATGTCCTTCAATTTGGCTTTGCTATAATGGTAGGCAATGCTGGTGCATCTTAGCCCTTT 120  
DB 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120

QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
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Db 301 TCTGTATATAACATGTGCTCCATCAGCTATGATGATACATCTGTCAGTCTCAAAATGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTTGG 420
Db 361 TCTTATAGAACTCAACATCTGGGGCTTGTGAAGATTTGCTCTGATGTGGCGCTTGG 420
Qy 421 ATACTGCTTCTTGGTAAATGGCCCGATGATCTGGCTTCAGATTTCTTGAAGAAACAGC 480
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Qy 481 ACGAACACAAGGACTCTGAGCCTGGCTTGTATACAGAGTGGTACATCCCTCACCAATTACA 540
Db 477 --TGAAGGTAGTGAATGGAACCTGGATTTTTCGGAATGGTACATCTCTGGCCATCACA 534
Qy 541 ATGCTCTTGGAAATCCCTGCTTCCGTCAATCTCTGTGCTTATTTCAATGTACAGATTTAC 600
Db 535 TCATTCTTGGAAATCTGTGATCCCGATCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
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Db 595 TGGAGCCTGTGGAAGCGTGTATCTCAGTAGGTGCCCAAGCCATCTGGAGTACTGCT 654
Qy 661 ACCTCTTCCAGTGTTCAGAGACATTAACAGAGCTGGGGTGGCTTCAGAGACAAGTAAT 720
Db 655 GTCTCTTCCAAACATCTGTGACACTCAATCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 721 CCTGGATTGAAGGAATCAGCTGCTATCTGTCACAGAAAGTCTCTCAAGAAAGAGAGCAGC 780
Db 715 TCTGCATTCGACGAAGTTCCTGCAATCCTTTCATTCAGAGAGACAGAGGAAGAGAGTAGT 774
Qy 781 ATCCTGGTGTCTTAAAGGATTCACATGAACAGACAGATATCACTGCTTCAAAAGTGGGTTC 840
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACATTTGCTTCCAAATAGGGTTCC 834
Qy 841 TTTCTGGCGATCGGAAGTGCAGGCTCTTCGCAAGAGGAGTAGCAGAGCTTCTCAGAGGC 900
Db 835 TTTCTCCCAATCAGATTCGTAGTCTTTCACCAAGGGAACATGTGAATCTGCTTAGAGCC 894
Qy 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTGTGTTGCTGGGCTCCA 954
Qy 961 TACTGTCTGTTTCAAAATGTCTTCAACTTACCCAGAAACGGAACGCCCAAAATCGGTG 1020
Db 955 TATTCTCTGTTCAAAATGTCTTCAATTTATTTCTCAGCAACAGGTCTCTAAATCAGTT 1014
Qy 1021 TGGTACAGCATTTGCTGCTGGTGAATGTTTCAATTCGTTTGTAAATCCCTTCTGTATC 1080
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Qy 1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140
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Qy 1141 CCAGCGCTGTACAGAAC---CAGTCAAGTATCTTCTGA 1176
Db 1135 CCTTCAACATCACACAGTGGTCAATCTCTTAA 1173
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RESULT 13

US-10-354-769-1

; Sequence 1, Application US/10354769

; Publication No. US20030149242A1

; GENERAL INFORMATION:

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; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-354-769-1
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Query Match 58.4%; Score 686.6; DB 7; Length 1173;

Best Local Similarity 75.1%; Pred. No. 4.7e-205;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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Qy 421 ATACTGCTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGAAGAAACAGC 480
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Qy 661 ACCTCTTCCAGTGTTCAGAGACATTAACAGAGTGGGGTGGCTTCAGAGACAAGTAAT 720
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QY 781 ATCCTGTGTCTTAAAGACTCAGTGAACAGCAGATATCACTGCTTTCAAAGTGGGTTC 840  
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATAGCAATGCTTCCAAAATGGGTTC 834  
QY 841 TTCTGGGATCGAAGATGAGGCTTCGGCAAGAGGAGTACGAGAGCTTCTCAGAGGC 900  
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCAACCAAGGGAACATGTGAACCTGCTTAGAGCC 894  
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Db 1135 CCTTACCATCACACACAGCTCGGTGAGTATCTTTAA 1173

## RESULT 14

US-10-393-807-13  
; Sequence 13 Application US/10393807  
; Publication No. US20030175891A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/393,807  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-393-807-13  
Query Match 58.4%; Score 686.6; DB 7; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 4,7e-205;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGGCCACACAGCTGCTCAGGTCCCTTTGGCATTT 60  
Db 1 ATGCCAGATCTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
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QY 601 TGGAGCTGTGGAAGCTTAGGGCTCTCAGTAGTGGCTTCCCTAGCCATGCTGATTTCTCCACT 660  
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QY 661 ACCTTTCAGTGTCTTACAGGACATTTACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720  
Db 655 GTCTCTTCCAAATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714  
QY 721 CCTGGATTGAGGAATCAGCTGCACTCTGTCATCTCAGAAAGTCTTCAAGAAAGAGCAGC 780  
Db 715 TCTGCACTCAGACAGAGTTTCTGTCATCTTTTCAATTCAGAGAGACAGAGAGAGTAGT 774  
QY 781 ATCCTGTGTCTTAAAGACTCAGATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 840  
Db 775 CTATGTTTCTCAGAACCAAGATGAATAGCAATACATTTGTTCCAAATAGGGTTC 834  
QY 841 TTCTGGCGATCGGAAAGTGCAGCGCTTTCGCCAAAGGAGTACGACAGAGCTTCTCAGAGGC 900  
Db 835 TTCTCCCAATCAGATCTCTGTAGCTTTCACCAAGGGAACATGTTGAATGCTTTAGAGCC 894  
QY 901 AGAAGCTAGCAGGTCACTGGCCATCTTCTCAGCGCTTTTCCCATTTTCTGGCTCCA 960  
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTTCTTAGGGGTTTTTGTGTTTCTGGGCTCCA 954  
QY 961 TACTGTCTGTTCACAATTTGTCCTTTCAACTTACCCAGAAAGGAAAGCCCAAAATCGGTG 1020



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Db 1015 TGGTATAGAATGCAATTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTTGTAT 1074  
Qy 1081 CCTTTGTTGTCACAGCGCTTTCCAGAAAGCTTTCTGGAAGATACCTTTGTGTACAAAGCAA 1140  
Db 1075 CCATTTGTTGTCACAGCGCTTTCAAAAGGCTTTCTTGAAATATATTTTGTATAAAAGCAA 1134  
Qy 1141 CCAGCGCTGTCACAGAAC---CAGTCAGTATCTCTTTGA 1176  
Db 1135 CCTTACCATCACACACAGTCGGTCAATCTCTTAA 1173

## RESULT 15

US-10-417-820A-13  
; Sequence 13, Application US/10417820A  
; Publication No. US20030229216A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lowitz, Kevin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7. US28.CON  
; CURRENT FILING NUMBER: US/10/417,820A  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-417-820A-13  
Query Match 58.4%; Score 686.6; DB 7; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 4,7e-205;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTCCACAGCTGCTCAGGTCCCTTGGCAATTT 60  
Db 1 ATGCCAGATACTAATAGCAATCAATTTATCACTAGCACTGCTGTACTTTAGCAATTT 60  
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GenCore version 5.1.8  
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Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 6: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	685	58.2	1173	7	US-11-242-505A-26
2	685	58.2	1265	7	US-11-242-505A-25
3	49.2	4.2	1847	6	US-10-511-937-2881
4	37.4	3.2	1105	7	US-11-312-958-23
5	35.2	3.0	1323	7	US-11-302-678-42
6	35.2	3.0	1984	7	US-11-302-678-40
7	35	3.0	50000	6	US-10-528-659-2
8	34.2	2.9	394191	6	US-10-506-549-3
9	34	2.9	2634	7	US-11-217-529-79043
c 10	33.8	2.9	5193	7	US-11-317-983-3
c 11	33.8	2.9	5339	7	US-11-317-983-24
12	33.6	2.9	1143	7	US-11-302-678-21
13	33.6	2.9	1182	7	US-11-302-678-19
c 14	33.4	2.8	300	7	US-11-217-529-81301
15	33.4	2.8	1074	7	US-11-302-678-39
16	33.4	2.8	1159	7	US-11-302-678-37
c 17	33	2.8	471	7	US-11-217-529-77805
c 18	33	2.8	2230	6	US-10-511-937-354
c 19	32.6	2.8	641	6	US-10-488-619-1577
20	32.6	2.8	1143	7	US-11-304-129-51
21	32.4	2.8	17569	7	US-11-301-554-1804
22	32	2.7	1266	7	US-11-304-129-46
23	31.8	2.7	1679	6	US-10-473-173-65
24	31.8	2.7	1679	6	US-10-505-928-746
25	31.8	2.7	1679	6	US-10-511-937-428

26	31.8	2.7	1679	6	US-10-511-937-2896	Sequence 2896, Ap
27	31.8	2.7	1679	6	US-10-511-937-2918	Sequence 2918, Ap
28	31.6	2.7	1152	7	US-11-304-129-35	Sequence 35, Appl
29	31.6	2.7	4052	7	US-11-312-958-5	Sequence 5, Appl
c 30	31.2	2.7	1716	7	US-11-217-529-77529	Sequence 77529, A
31	31	2.6	1179	7	US-11-304-129-50	Sequence 50, Appl
c 32	30.6	2.6	645	7	US-11-217-529-174509	Sequence 174509, Ap
c 33	30.6	2.6	783	7	US-11-217-529-5199	Sequence 5199, Ap
c 34	30.6	2.6	1506	7	US-11-217-529-1627	Sequence 1627, Ap
c 35	30.4	2.6	3003	6	US-10-196-749-51	Sequence 51, Appl
c 36	30.4	2.6	3651	7	US-11-217-529-75679	Sequence 75679, A
c 37	30.4	2.6	50000	6	US-10-528-659-2	Sequence 2, Appl
38	30.2	2.6	396	7	US-11-217-529-5853	Sequence 5853, Ap
c 39	30.2	2.6	724	6	US-10-488-619-1649	Sequence 1649, Ap
c 40	30.2	2.6	1476	7	US-11-217-529-917	Sequence 917, App
c 41	30.2	2.6	1653	7	US-11-217-529-81987	Sequence 81987, A
c 42	30.2	2.6	1704	7	US-11-217-529-79816	Sequence 79816, A
c 43	30	2.6	742	6	US-10-511-937-2887	Sequence 2887, Ap
c 44	30	2.6	1837	6	US-10-511-937-537	Sequence 537, App
c 45	30	2.6	1837	6	US-10-516-478-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-11-242-505A-26  
; Sequence 26, Application US/11242505A  
; Publication No. US2006009656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, c  
; FILE REFERENCE: MPI2001-288P/RCP/OWNIM  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1173)  
US-11-242-505A-26

Query Match	58.2%	Score 685;	DB 7;	Length 1173;
Best Local Similarity	75.1%	Pred No. 2,9e-209;		
Matches 885;	Conservative 0;	Mismatches 285;	Indels 9;	Gaps 2;
Qy	1	ATGTGGAGTCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGTCCCTTGGCATTT	60	
Db	1	ATGCCAGATCTAATAGCACAATCAATTTATCCTAACGACCTCGTGTACTTTAGCATTT	60	
Qy	61	TTAATGCTTTCATTTGCCCTTTGCTATATGTTAGGCAATGCTGTGCTATCTTAGCCTTT	120	
Db	61	TTTATGCTTTCATTTAGCTTTTGTCTATATGTTAGGCAATGCTGTGCTATCTTAGCCTTT	120	
Qy	121	GTGTGGACAGAACTTAGACATCGAAGTAAATTTTTTCTTAATTTGGCTATTTCT	180	
Db	121	GTGTGGACAAACCTTAGACATCGAAGTAAATTTTTTCTTAATTTGGCTATTTCT	180	

GENERAL INFORMATION:	
; APPLICANT: Carroll, Joseph M.	
; APPLICANT: Healy, Aileen	
; TITLE OF INVENTION: Methods and Compositions for Treating	
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,	
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,	
; FILE REFERENCE: MPI2001-288P/RCP/OWNIM	
; CURRENT APPLICATION NUMBER: US/11/242,505A	
; CURRENT FILING DATE: 2005-10-03	
; PRIOR APPLICATION NUMBER: US 10/290,078	
; PRIOR FILING DATE: 2002-11-07	
; PRIOR APPLICATION NUMBER: US 60/347,949	
; PRIOR FILING DATE: 2001-11-07	
; PRIOR APPLICATION NUMBER: US 10/320,351	
; PRIOR FILING DATE: 2002-12-16	
; PRIOR APPLICATION NUMBER: 60/341,606	
; PRIOR FILING DATE: 2001-12-17	
; NUMBER OF SEQ ID NOS: 48	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 25	
; LENGTH: 1265	
; TYPE: DNA	
; ORGANISM: Homo Sapiens	
US-11-242-505A-25	
Query Match 58.2%; Score 685; DB 7; Length 1265;	
Best Local Similarity 75.1%; Pred. No. 3.1e-209; Indels 9; Gaps 2;	
Matches 885; Conservative 0; Mismatches 285;	
QY 1 ATGTCGGAGTCTAAACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCCTTGGCATTTT 60	
DB 55 ATGCCAGATCTAATAGACAAATCAATTTATCATAAGCACATCGTTACTTTAGCATTT 114	
QY 61 TTAATGTCCTTCAATTTGCCCTTGTCTATAATAGTGAAGCAATGCTGTGTCATCTTAGCTTT 120	
DB 115 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCACTTTTAGCTTTT 174	
QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180	
DB 175 GTGTGGACAGAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCTATTTCT 234	
QY 181 GACTTCTCGTGGTGTGATTTTCCATTTCTGTATACATCCCTCACGCTGTGTTAACTGG 240	
DB 235 GACTTCTTGTGGTGTGATTTTCCATTTCTGTATACATCCCTCACGCTGTGTTAACTGG 294	
QY 241 AATTTTGAAGTGGAAATCTGCATGTTTTTGGCTCATCTACTGACTATCTTTTGTGTCACGCA 300	
DB 295 GATTTTGGAAAGGAAATCTGTGTAATTTGGCTCACTACTGACTATCTGTATGTACAGCA 354	
QY 301 TCTGTCTACAATATTTGCTCTCATTTAGCTAGATCGATACAGTCAGTCAGTTTCAAATGCTGTG 360	
DB 355 TCTGTATATAACAAATGTCTCTCATCTAGATGATCGATACCTGTCACTCAAAATGCTGTG 414	
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTGG 420	
DB 415 TCTTATAGAACTCAACATCTAGTGGGCTTTGAAGATTGTTACTCTGATGGTGGTGGTGG 474	
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480	
DB 475 GTGCTGGCTTCTTCTAGTGAATGGCCCAATGATTTCTAGTTTTCAGAGTCTTGAAGGA --- 530	
QY 481 ACGAACACAAAGACTGTGAGCCCTGGCTTTGTACAGAGTGGTACATCTCCATCACCATTACA 540	
DB 531 --TGAAGGTAGTGAATGAACTGGACCTGGATTTTTTTCGGAATGGTACATCTTGGCATCACA 588	
QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCTCATCTCTGTGGCTTTATTTCAATGTACAGATTAC 600	
DB 589 TCATTTCTTGAATTCGTGATCCCGAGTCATCTTAGTCGCTTATTTTCAACATGAATATTTAT 648	
QY 601 TGGAGCCTGTGGAAGCGGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTTCTCCACT 660	
DB 649 TGGAGCCTGTGGAAGCGGTAGGTCTCTCAGTAGGTGCCCAAGCCATCTCTGGAGTACTGCT 708	

QY 181 GACTTCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACTGG 240	
DB 181 GACTTCTTGTGGTGTGATTCCTATTCCTTTGTACATCCCTCACACGCTGTTCGAATGG 240	
QY 241 AATTTTGAAGTGGAAATCTGCATGTTTTTGGCTCATCTACTGACTATCTTTTGTGACCGCA 300	
DB 241 GATTTTGAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300	
QY 301 TCTGTCTACAATATTTGCTCTCATTTAGCTAGATCGATACAGTCAGTCAGTTTCAAATGCTGTG 360	
DB 301 TCTGTATATAACAAATGTCTCTCATCTAGTGGGCTTTGAAGATTGTTACTCTGATGGTGGTGGTGG 420	
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGTCTCAAAATGGTGGCTGTTTGG 420	
DB 361 TCTTATAGAACTCAACATCTAGTGGGCTCTTGAAGATTGTTACTCTGATGGTGGTGGTGGTGG 420	
QY 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480	
DB 421 GTGCTGGCTTCTTAGTGAATGGCCCAATGATTTCTAGTTTTCAGAGTCTTGAAGGA --- 476	
QY 481 ACGAACACAAAGACTGTGAGCTCGCTTGTGTACAGAGTGTGATCATCTCCATCATTACA 540	
DB 477 --TGAAGGTAGTGAATGAACTGGATTTTTCGGAATGATGATCTCTTCCCATCACA 534	
QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCTCATCTCTGTGGCTTTATTTCAAATGTACAGATTAC 600	
DB 535 TCATTTCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTTTATTTCAAACATGAATATTTAT 594	
QY 601 TGGAGCCTGTGGAAGCGGTCTCAGTAGTGGCCCTAGCCATGCTGATTTCTCCACT 660	
DB 595 TGGAGCCTGTGGAAGCGGTCTCAGTAGTGGCCCAAGCCATCTCTGGACTGACTGCT 654	
QY 661 ACCTCTTCCAGTGTCTCAGACACTTACACAGAGCTGGGGTGGCTTGACAGCAAGTAAT 720	
DB 655 GTCTCTTCCAACATCTGTGGACACTCTTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714	
QY 721 CTTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTCGAAAGAAAGACGAGC 780	
DB 715 TCTGCATCAACAGAAAGTCTCTGCATCTTTCATTTACAGAGAGCGGAGGAGAAAGTAGT 774	
QY 781 ATCTGGTGTCTTAAAGACTCAATGAACAGCAGATATCACTGCTTTCAAAGTGGGTTC 840	
DB 775 CTATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834	
QY 841 TTTCTGGGATCGAAGTGCAGCGCTTCGCAAGGAGGTACGACAGCTTCTCAGAGGC 900	
DB 835 TTTCTCCCAATCAGATCTGTAGTCTTTCACCAAGGGAACATGTTGAACTGCTTAGAGCC 894	
QY 901 AGGAAGCTAGCCAGGTCACCTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGTCCA 960	
DB 895 AGGAGATTAGCCCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGTCCA 954	
QY 961 TACTGTCTGTTCACAAATGTTCCTTCACTTACCCAGAACGCAAGCCCAATCGGTG 1020	
DB 955 TATTCTCTGTTCACAAATGTTCCTTCAATTTATTTCTCAGCAACAGGTCTCAAAATCAGTT 1014	
QY 1021 TGGTACAGCAATTCCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTATC 1080	
DB 1015 TGGTATAGAAATGCAATTTTGGCTTCAGTGGTTCAATTCCTTGTCAATCTCTTTTGTAT 1074	
QY 1081 CCTTTGTGTACAGCGGCTTTCCAGAAAGGCTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140	
DB 1075 CCATTGTGTACAGCGCTTTTCAAAAGGCTTTCTTGAAGAAATATTTTGTATAAAAAGCAA 1134	
QY 1141 CCAGCGCTGTACAGAAC ---CAGTCAATCTTCTTGA 1176	
DB 1135 CCTTACCATCAACAACAGTCGGTCAAGTATCTTCTTAA 1173	

RESULT 2  
US-11-242-505A-25  
; Sequence 25, Application US/11242505A  
; Publication No. US2006009965A1

Qy	89	TGGTAGGCAATGCTGTGGTGCATCTTAGCGCTTTGGTGGACAGAAACCTTAGACATCGAA	148
Db	623	TTGCTGGCAATGTGGTGTCTGTCTGGCCGTGGGCTTGAACCGCGGGCTCCGCAACCTGA	682
Qy	149	GTAATTAATTTTTCTTAAATTTGGCTATTCTGACTCTCTCGTGGTGTGATTTCCATTC	208
Db	683	CCAAATGTTTCATCGTGTCCCTTGGCTATCATGACCTGCTCTCGGCCCTCTGGTGCTGC	742
Qy	209	CTCTGT---ACATCCCTCACGTGTGTTTAACTGGAATTTTGGAAAGTGGAAATCTGCATGT	265
Db	743	CGTTCTCTGCCATCTACAGCTGCTCGCAAGTGGAGCTTTGGCAAGGTCTTCTGCAATA	802
Qy	266	TTTGGCTCATTTACTGACTATCTTTTGTGCACGGCATCTGTCTACAAATATGTGTCCTCATTA	325
Db	803	TCTACACAGCGCTGGATGTAAGTCTTCTGCACAGCCTCCATCTTTAACTCTTCAATGATCA	862
Qy	326	GCTACGATCGATACAGTCACT	347
Db	863	GCCTCGACGGTACTGGGCTCT	884

RESULT 4  
US-11-312-958-23

US-11-312598-23  
Sequence 23, Application US/11312958  
Publication No. US20060100152A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Rosenfeld, Julie Beth  
APPLICANT: Silos-Santiago, Immaculada  
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,  
12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,  
27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,  
95431, 22425, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR  
13424 MOLECULES  
FILE REFERENCE: MPI02-027PIRNONNIM  
CURRENT APPLICATION NUMBER: US/11/312.958

Query Match	3.2%	Score 37.4;	DB 7;	Length 1105;
Best Local Similarity	53.0%	Pred. No. 0.019;		
Matches 80: Conservative		0: Mismatches	71: Indels	Gaps 0

Query Match 3.2%: Score 37.4: DB 7: Length 1105:

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QY 89 TGGTAGCAATGCTGGTTCATCTTAGCCTTTGTGGTGACAGAAACCTTAGACATCGAA 148
Db 176 TCGTGGCAACCTCCTGGTGATCTCTCCGCTCAGAAACCGAAGCTCCGGAACGCAG 235
QY 149 GTAATTATTTTTTTCTTAATTTGGCTATTTCTGACATTCCTCGTGGGTTTGATTTCCATTC 208
Db 236 GTAATTGTTCTTGGTGAGTCTGGCATTTGCTGACCTGGTGGTGGCTTCTACCCCTACC 295
QY 209 CTCGTACATCCCTCAGCTGTGTTGTTAACTG 239
Db 296 CGCTAATCCTCGTGGCCATCTTCTATGACGG 326

RESULT 5
US-11-302-678-42
; Sequence 42, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1323)
US-11-302-678-42

Query Match 3.0%; Score 35.2; DB 7; Length 1323;
Best Local Similarity 54.8%; Pred. No. 0.11;
Matches 92; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 178 TCTGACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTGTTT 234
Db 211 TCTGACCTGATGGTGGGCTGGTGGTGATGCGCGGCCCATGCTGAAACGGCGCTACGGG 270
QY 235 AACTGGAATTTTGAAGTGAATCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGC 294
Db 271 CGTGGGTGCTGGCGCGGCGCTCTGCTGTCTGAGCCGCGCTTCGACGATGATGTGCTGC 330
QY 295 ACCGCACTCTGTACAATATTGTCTCATTTAGCTACGATCGATACCGAG 342
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Db 331 AGCGCCTCCATCCTCAACCTCTGCTCATCGCCTGACCGCTACCTG 378

RESULT 6
US-11-302-678-40
; Sequence 40, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (468)...(1790)
US-11-302-678-40

Query Match 3.0%; Score 35.2; DB 7; Length 1984;
Best Local Similarity 54.8%; Pred. No. 0.14;
Matches 92; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 178 TCTGACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTGTTT 234
Db 678 TCTGACCTGATGGTGGGCTGGTGGTGATGCGCGGCCCATGCTGAAACGGCGCTACGGG 737
QY 235 AACTGGAATTTTGAAGTGAATCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGC 294
Db 738 CGTGGGTGCTGGCGCGGCGCTCTGCTGTCTGAGCCGCGCTTCGACGATGATGTGCTGC 797
QY 295 ACCGCACTCTGTACAATATTGTCTCATTTAGCTACGATCGATACCGAG 342
Db 798 AGCGCCTCCATCCCTCAACCTCTGCTCATCGCCTGACCGCTACCTG 845

RESULT 7
US-10-528-659-2
; Sequence 2, Application US/10528659
; Publication No. US2006009594A1
; GENERAL INFORMATION:
; APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
```

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; APPLICANT: GIFU INTERNATIONAL INSTITUTE OF BIOTECHNOLOGY
; APPLICANT: YAMADA, Yoshiji
; APPLICANT: YOKOTA, Mitsuhiro
; TITLE OF INVENTION: Method for diagnosing a risk of hypertension
; FILE REFERENCE: C0200701
; CURRENT APPLICATION NUMBER: US/10/528,659
; CURRENT FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: JP P2002-280034
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-528-659-2

Query Match          3.0%; Score 35; DB 6; Length 50000;
Best Local Similarity 48.0%; Pred. No. 1.2; Indels 3; Gaps 1;
Matches 132; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

Qy      89  TGGTAGGCAATGCTGTGCTCATCTTAGCCCTTTGTGGTGGACAGAAACCTTAGACATCGAA 148
Db      46275 TTGTGGCAACATGCTGGTCTCTCATCTTAATAAACTGCAAAAGCTGAAGTCTTGA 46334

Qy      149  GTAATTAATTTTCTTAATTTGCTATTTCTGACTTCTCTCGTGGGTTTGAATTTCCATTC 208
Db      46335 CTGACATTTACCTGCTCAACCTGCCATCTCTGATCTGCTTTT---TCTTATTACTCTCC 46391

Qy      209  CTCGTGATACCTCCACGTGTGTTTAACTGGAATTTTGGAGTGGATCGCATGTTTT 268
Db      46392 CATTTGGGCTCACTCTGCTGCAAAATGAGTGGGCTTTTGGGAATGCAATGCAAAATAT 46451

Qy      269  GGCTCAATTACTGACTATCTTTTGTGCAACGCACTCTGCTCAAAATATGCTCAATTAGCT 328
Db      46452 TCACAGGGCTATACATCGTTATTTTGGCGGAATCTTTCATCATCTCTCTGCAA 46511

Qy      329  ACGATGATACCACTGATGATTTCAAAATGCTGTGTTCT 363
Db      46512 TCGATAGATACCTGGCTATTGCTCAATGCTGTGTTT 46546

-
RESULT 8
US-10-506-549-3
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CL001361-US
; CURRENT APPLICATION NUMBER: US/10/506,549
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/361,343
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 394191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(394191)
; OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match          2.9%; Score 34.2; DB 6; Length 394191;
Best Local Similarity 55.5%; Pred. No. 7.7; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy      66  GTCTTCATTTGGCCTTTGCTATATAGGTAGGCAATGCTGTGTCATCTTAGCCCTTTGGT 125

; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79043
; LENGTH: 2634
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79043

Query Match          2.9%; Score 34; DB 7; Length 2634;
Best Local Similarity 48.9%; Pred. No. 0.4; Indels 0; Gaps 0;
Matches 91; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy      79  TTGCTATAATGGTAGGCAATGCTGTGTCATCTTAGCCCTTTGTGGTGGACAGAAACCTT 138
Db      1678 TTTGCCATATTGATAGGCTCACTTGTGTGGAATAGCTGTTGTAGAGCACTACCCAACA 1737

Qy      139  AGACATCGAAGTAATTAATTTTCTTAATTTTGGCTATTTCTGACTTCTCTCGGTTTG 198
Db      1738 AATACACCAAGTTTGGGGTCTTTTGTGTTAGGAATTAATTTGTTTCTTGATCCA 1797

Qy      199  ATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTTAACCTGGAATTTTGGAGTGAATC 258
Db      1798 ACTACTATCTTCAAGCAACCACTGGTTTTCGTTTGGTTTGAATCTACTAATGAAATG 1857

Qy      259  TGCATG 264
Db      1858 GTGATG 1863

RESULT 10
US-11-317-983-3/c
; Sequence 3, Application US/11317983
; Publication No. US2006090222A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Jako, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684.US
; CURRENT APPLICATION NUMBER: US/11/317,983
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/11/117,005
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1999-12-16

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; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5193
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-317-983-3

Query Match      2.9%; Score 33.8; DB 7; Length 5193;
Best Local Similarity 58.4%; Pred. No. 0.72;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 156 TTTTCTTAAATTTGGCTATTTCTGACTTCCTCGTGGTTTGATTTCCATTCCTCTGTA 215
Db 1355 TTTTCTTAAATTTGGCTATTTCTGACTTCCTCGTGGTTTGATTTCCATTCCTCTGTA 215

Qy 216 CATCCCTCACGTGTTGTTAACTGGAATTTTGGAAAGTGGAA 256
Db 1295 CTATATTGAGTGTTTTTTAGTGAATATTTTAAGAAGAA 1255

RESULT 11
US-11-317-983-24/c
; Sequence 24, Application US/11317983
; Publication No. US2006009022A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Jako, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684.1US
; CURRENT APPLICATION NUMBER: US/11/317,983
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/11/117,005
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 5339
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-317-983-24

Query Match      2.9%; Score 33.8; DB 7; Length 5339;
Best Local Similarity 58.4%; Pred. No. 0.73;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 156 TTTTCTTAAATTTGGCTATTTCTGACTTCCTCGTGGTTTGATTTCCATTCCTCTGTA 215
Db 1355 TTTTCTTAAATTTGGCTATTTCTGACTTCCTCGTGGTTTGATTTCCATTCCTCTGTA 215

Qy 216 CATCCCTCACGTGTTGTTAACTGGAATTTTGGAAAGTGGAA 256
Db 1295 CTATATTGAGTGTTTTTTAGTGAATATTTTAAGAAGAA 1255

RESULT 12
US-11-302-678-21
; Sequence 21, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; NUMBER OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM.OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1143)
US-11-302-678-21

Query Match      2.9%; Score 33.6; DB 7; Length 1143;
Best Local Similarity 45.2%; Pred. No. 0.32;
Matches 123; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 89 TGTAGGCAATGCTGTGTCATCTTAGCCCTTTGTGGTGACAGAACTTAGACATCGAA 148
Db 221 TGTGGGCAACTCGTGTGTCATGTCGTATCATCCGATACACAAAGATGAAGACAGAA 280

Qy 149 GTAATATTTTTTCTTAATTTGGCTATTTCTGATCTTCCTCGTGGGTTTGTATTCATTC 208
Db 281 CCAACATTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACCAACCGCCT 340

Qy 209 CTCTGTATATCCCTCACGTGTTGTTAACTGGAATTTTGGAAAGTGAATCTGCAATGTTTT 268
Db 341 TTAGAGTACGGTCTACTTGTATGAAATCTTGGCCCTTTTGGGATGTCTGTGCAAGATAG 400

Qy 269 GGCTCAATTAAGTACTATPCTTTTGTGACCGCATCTGTCTCAATATTTGCTCTCATAGCT 328
Db 401 TAAATTTCCATTGATTACTACAAACATGTTCCACGACATCTTCACCTTGACCATGATGACG 460

Qy 329 AGATCATACAGTCAAGTTCAGTTTCAAAATGCTGTG 360
Db 461 TGGACCGCTACATTTGCCGTGTGCCACCCCGTG 492

RESULT 13
US-11-302-678-19
; Sequence 19, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
```



; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323.  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MPI02-012PIRNM.OMNI  
; CURRENT APPLICATION NUMBER: US/11/302,678  
; CURRENT FILING DATE: 2005-12-14  
; PRIOR APPLICATION NUMBER: US/10/345,680  
; PRIOR FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 1182  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (14)...(1156)  
US-11-302-678-19

Query Match 2.9%; Score 33.6; DB 7; Length 1182;  
Best Local Similarity 45.2%; Pred. No. 0.33; Indels 0; Gaps 0;  
Matches 123; Conservative 0; Mismatches 149

QY	89	TGGTAGCAATGCTGTGCTATCTTAGCTTTGGTGGACAGAAACCTTAGACATCGAA	148
Db	234	TGGTGGCACTCGCTGGTATGTCGTGATCATCCGATACACAAATGAGACACAA	293
QY	149	GTAATTAATTTTCTTAATTTGGCTATTTCTGACTTCTCGTGGGTTGATTTCCATTC	208
Db	294	CCAACATTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCT	353
QY	209	CTCTGTACATCCCTCAGCTGTGTTTAACTGGAATTTTGGAGTGGAACTGCAATGTTT	268
Db	354	TTCAAGATACGGTCTACTTGTATGAATTCCTGGCCCTTTTGGGGATGCTGTGCAAGATAG	413
QY	269	GGCTCAATTAAGTACTATCTTTTGGACCGCATCTGTCTCAATATTTGCTCAATAGCT	328
Db	414	TAATTTCCATTTGATTTACACATGTTTCCAGCATCTTCCCTTGACCATGATGAGCG	473
QY	329	ACCATGATACCATGCTAGTTTCAATATGCTGTG	360
Db	474	TGGACCGCTACATTTGCCGTGTGCCACCCCGTG	505

RESULT 14  
US-11-217-529-81301/c  
; Sequence 81301, Application US/11217529  
; Publication No. US2006099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 81301  
; LENGTH: 300  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-81301

Query Match 2.8%; Score 33.4; DB 7; Length 300;  
Best Local Similarity 48.7%; Pred. No. 0.16;  
Matches 91; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY	402	TCAAATGCTGCTGTTGGATACCTGCTTTCTTGTAAATGCCCGATGATTTCTGGCTTC	461
Db	300	TCATCTGATTCGTTGTTGAATAATGCTGCTTTTCAATAGCGCAATTTTGTCTCTTC	241
QY	462	AGATTTCTTGAAGAACACAGACGACACAAAGGACTGTGAGCCTGGCTTTGTACAGATG	521
Db	240	GAAATCTTCAAAGTAAAGCTCTCTCGTTATTATAGATAGATATCAACCTACGAAGC	181
QY	522	GTACATCCTCACCATTACAAATGCTTTGGAAATTCCTGCTCTCTCATCTCTGTGGCTTA	581
Db	180	GACAAATGAGGCATATAAACAATTTCTTCTTGAATACTGACTCTTTTCCAAATCTTTCCA	121
QY	582	TTTCAAT 588	
Db	120	ATCAAT 114	

RESULT 15

US-11-302-678-39  
; Sequence 39, Application US/11302678  
; Publication No. US2006089881A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MPI02-012PIRNM.OMNI  
; CURRENT APPLICATION NUMBER: US/11/302,678  
; CURRENT FILING DATE: 2005-12-14  
; PRIOR APPLICATION NUMBER: US/10/345,680  
; PRIOR FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 39  
; LENGTH: 1074



GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 24, 2006, 13:31:49 ; Search time 195 Seconds  
(without alignments)  
916.778 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
Sequence: 1 MSSNSTGILPPAAQVPLAF.....WKILCVTKWPAISONQSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2035	99.4	391	5	AAM50565 Mouse his
2	2035	99.4	391	8	ADO29497 Mouse GPC
3	1745	85.2	391	5	AAM50566 Rat hist
4	1370.5	66.9	390	3	AAB02831 Human G p
5	1370.5	66.9	390	3	AAY71297 Human orp
6	1370.5	66.9	390	4	AAB62445 Human GPC
7	1370.5	66.9	390	4	AAG64477 Human G p
8	1370.5	66.9	390	4	AAB73622 Human G p
9	1370.5	66.9	390	5	AAM53050 Human G p
10	1370.5	66.9	390	5	ABP98629 Human his
11	1370.5	66.9	390	5	ABB78276 Amino aci
12	1370.5	66.9	390	5	AAM50564 Human his
13	1370.5	66.9	390	5	AAG66023 Human his
14	1370.5	66.9	390	5	Aau74906 Amino aci
15	1370.5	66.9	390	6	ABG71960 Human G-p
16	1370.5	66.9	390	6	ABU92265 Human G p
17	1370.5	66.9	390	6	ABP81727 Human his
18	1370.5	66.9	390	6	Aae36417 Human H4
19	1370.5	66.9	390	7	ADG98760 Human orp
20	1370.5	66.9	390	7	ADJ26923 Human end
21	1370.5	66.9	390	8	ADG86375 Human end
22	1370.5	66.9	390	8	ADJ88376 Novel hum
23	1370.5	66.9	390	8	ADO05720 Human his

24	1370.5	66.9	390	8	ADO29496	Ado29496 Human GPC
25	1370.5	66.9	390	8	ADP20168	Adp20168 Human G p
26	1370.5	66.9	390	8	ADQ75074	Adq75074 Human G p
27	1370.5	66.9	390	9	ADY86900	Ady86900 Human his
28	1370.5	66.9	391	5	AAM53052	Aam53052 Human G p
29	1370.5	66.9	392	5	AAM53053	Aam53053 Human G p
30	1366.5	66.7	390	4	AAM51410	Aam51410 Human GPR
31	1366.5	66.7	390	6	AAE36416	Aae36416 Human H4
32	1365.5	66.7	390	8	ADG86522	Adg86522 Guinea end
33	1238	60.4	389	5	AAM50567	Aam50567 Guinea pi
34	1198	58.5	357	6	AAE36415	Aae36415 Human H4
35	1074.5	52.5	336	6	AAE36414	Aae36414 Human H4
36	1064	52.0	649	8	ADU82861	Adu82861 Ligand up
37	729.5	35.6	415	7	RAO29530	Aao29530 Human H3
38	722.5	35.3	445	2	AAW92975	Aaw92975 Human mAC
39	722.5	35.3	445	2	AAAY06322	Aay06322 Human G p
40	722.5	35.3	445	2	AAAG67830	Aag67830 Human mus
41	722.5	35.3	445	3	AAAY92218	Aay92218 Human his
42	722.5	35.3	445	4	AAAB30627	Abb30627 A human h
43	722.5	35.3	445	5	ABBB79792	Abb79792 Human his
44	722.5	35.3	445	6	ABRA43667	Abra43667 Human his
45	722.5	35.3	445	6	ABP57425	Abp57425 Human his

ALIGNMENTS

RESULT 1  
AAM50565  
ID AAM50565 standard; protein; 391 AA.  
XX  
AC AAM50565;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Mouse histamine H4 receptor.  
XX  
KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.  
XX  
OS Mus musculus.  
XX  
FN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX Lovenberg T, Liu C;  
XX WPI; 2002-114339/15.  
XX N-PSDB; AAI70981.  
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is  
PT beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
XX Claim 13; Fig 5B; 92pp; English.  
CC The present sequence is that of a mouse histamine receptor of the H4  
CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA  
CC library. The invention provides mammalian (human, mouse, rat and guinea  
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4

CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the histamine H4 receptor. Such modulators may be useful  
CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
CC the neuroendocrine system, stress and spasticity

XX  
SQ Sequence 391 AA;  
Query Match 99.4%; Score 2035; DB 5; Length 391;  
Best Local Similarity 99.7%; Pred. No. 8.2e-202;  
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSESNTGILPPAAQVPLAFIMSFAPAIMVGNVILAFVDRNLHRHSNYFFLNLAIS 60  
DB 1 MSESNTGILPPAAQVPLAFIMSFAPAIMVGNVILAFVDRNLHRHSNYFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHYLFWNNFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120  
DB 61 DFLVGLISIPLYIPHYLFWNNFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120  
QY 121 SYRAQHTGIMKIIVAQMVAVVILAFVNGPMLASDSWKNSTNTKDCPFGVTEWYILITIT 180  
DB 121 SYRAQHTGIMKIIVAQMVAVVILAFVNGPMLASDSWKNSTNTKDCPFGVTEWYILITIT 180  
QY 181 MLEFFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACTSN 240  
DB 181 MLEFFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACTSN 240  
QY 241 PGLKESAASHRSPPRRKSSILVSLRTHMNSSITAFKVGFWRSSEALRQREYAEILLRG 300  
DB 241 PGLKESAASHRSPPRRKSSILVSLRTHMNSSITAFKVGFWRSSEALRQREYAEILLRG 300  
QY 301 RKLARSAILLSFAICWAPCYCLFTVLSTYPRTERPKSVWYSTAFWLFNFSFVNPFLY 360  
DB 301 RKLARSAILLSFAICWAPCYCLFTVLSTYPRTERPKSVWYSTAFWLFNFSFVNPFLY 360  
QY 361 PLCHRRFQKAFKILCVTKPALSQNSQSVS 391  
DB 361 PLCHRRFQKAFKILCVTKPALSQNSQSVS 391

RESULT 2

AD029497  
ID ADO29497 standard; protein; 391 AA.  
XX  
AC ADO29497;  
XX  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Mouse GPCR HRH4, SEQ ID NO:599.  
XX  
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;  
KW cytosolic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;  
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
KW murine; receptor.  
XX  
OS Mus musculus.  
XX  
PN WO2004040000-A2.  
XX  
PD 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.  
XX  
XX  
PR 09-SEP-2002; 2002US-0409303P.  
PR 09-APR-2003; 2003US-0461329P.  
XX  
XX (PRIM-) PRIMAL INC.  
XX  
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
XX  
XX WPI; 2004-390329/36.  
DR N-PSDB; ADO30257.  
XX  
XX Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
XX  
XX  
PS Claim 151; SEQ ID NO 599; 542pp; English.  
XX  
XX The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridize to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., osteoarthritis, rheumatoid  
CC AIDS); bone and joint disorders (e.g., osteoporosis); metabolic or nutritive disorders (e.g.,  
CC arthritis, gout or osteoporosis); metabolic or nutritive deficiency-related  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
CC invention. Note: The full sequence data for this patent did not form part  
CC of the printed specification; those sequences not shown were obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 391 AA;  
Query Match 99.4%; Score 2035; DB 8; Length 391;  
Best Local Similarity 99.7%; Pred. No. 8.2e-202;  
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSESNTGILPPAAQVPLAFIMSFAPAIMVGNVILAFVDRNLHRHSNYFFLNLAIS 60  
DB 1 MSESNTGILPPAAQVPLAFIMSFAPAIMVGNVILAFVDRNLHRHSNYFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHYLFWNNFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120  
DB 61 DFLVGLISIPLYIPHYLFWNNFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120  
QY 121 SYRAQHTGIMKIIVAQMVAVVILAFVNGPMLASDSWKNSTNTKDCPFGVTEWYILITIT 180  
DB 121 SYRAQHTGIMKIIVAQMVAVVILAFVNGPMLASDSWKNSTNTKDCPFGVTEWYILITIT 180  
QY 181 MLEFFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACTSN 240  
DB 181 MLEFFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACTSN 240

Db 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSPHAGSTTSSASGHLHRAGVACRTSN 240  
 Qy 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEALLRG 300  
 Db 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEALLRG 300  
 Qy 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360  
 Db 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360  
 Qy 361 PLCHRRFPQKAFWKILCVTKWPALSONQSVSS 391  
 Db 361 PLCHRRFPQKAFWKILCVTKWPALSONQSVSS 391

RESULT 3  
 AAM50566  
 ID AAM50566 standard; protein; 391 AA.  
 XX  
 AC AAM50566;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE Rat histamine H4 receptor.  
 XX  
 KW Histamine H4 receptor; rat; antidiarrhetic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy.  
 XX  
 OS Rattus rattus.  
 XX  
 PN WO200192485-A1.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US005914.  
 XX  
 PR 31-MAY-2000; 2000US-0208260P.  
 XX  
 PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX  
 PI Lovenberg T, Liu C;  
 XX  
 DR WPI; 2002-114339/15.  
 XX  
 PR N-PSDB; AAI70982.  
 XX  
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 PS Claim 13; Fig 6A; 92pp; English.  
 XX  
 CC The present sequence is that of a rat histamine receptor of the H4  
 CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA  
 CC library. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the histamine H4 receptor. Such modulators may be useful  
 CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
 CC the neuroendocrine system, stress and spasticity

Sequence 391 AA;  
 Query Match 85.2%; Score 1745; DB 5; Length 391;  
 Best Local Similarity 84.9%; Pred. No. 9.6e-172;  
 Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MSESNTGIIIPPAQVPLAFMLMSFAFAIMVGNVAVILAFVVDRLNRHRSNYFFLNLAIS 60  
 Db 1 MSESNGTDVLPFLTAQVPLAFMLSLFAITIGNAVILAFVADRLNRHRSNYFFLNLAIS 60  
 Qy 61 DFLVGLISIPLYIPIHVLFNMFSGGICMFWLITDYLCTASVYNIVLISYDRYOSVSNV 120  
 Db 61 DFFVGVISIPLYIPIHVLFNMFSGGICMFWLITDYLCTASVYNIVLISYDRYOSVSNV 120  
 Qy 121 SYRAQHTGIMKIIVAQMVAVMILAFVNGPMLASDSWKNSNTKDCBPGFVTEWYILIT 180  
 Db 121 RYRAQHTGILKIIVAQMVAVMILAFVNGPMLASDSWKNSNTKDCBPGFVTEWYILIT 180  
 Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSPHAGSTTSSASGHLHRAGVACRTSN 240  
 Db 181 AFLEFLLPVSLVYFVSQIYWSLWKRGSLSRCPSPHAGFIATSSRGTHSRRTGLACRTSL 240  
 Qy 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEALLRG 300  
 Db 241 PGLKEPAASHSESPPRGKSSLLVSLRTHMSSIIAFKVGSPCRSESPVLLHQREHVELLRG 300  
 Qy 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360  
 Db 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFY 360  
 Qy 361 PLCHRRFPQKAFWKILCVTKWPALSONQSVSS 391  
 Db 361 PLCHRRFPQKAFWKILCVTKQAPSPQTSQSVSS 391

RESULT 4  
 AAB02831  
 ID AAB02831 standard; protein; 390 AA.  
 XX  
 AC AAB02831;  
 XX  
 DT 22-AUG-2000 (first entry)  
 XX  
 DE Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.  
 XX  
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;  
 KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200022131-A2.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 13-OCT-1999; 99WO-US024065.  
 XX  
 PR 13-OCT-1998; 98US-00170496.  
 PR 12-NOV-1998; 98US-0108029P.  
 PR 20-NOV-1998; 98US-0109213P.  
 PR 17-NOV-1998; 98US-0110060P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123944P.  
 PR 12-MAR-1999; 99US-0123945P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123948P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 28-MAY-1999; 99US-0137567P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 27-AUG-1999; 99US-0151114P.  
 PR 03-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.



Qy 1 MSENSTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNLRHSNYFFLNLAIS 60  
Db 1 MPDNTNINSLSTRVTLAFFMSLVAFAMLGNALVILAFVVDKLNLRHSNYFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPHLVFNNGSGICMFWMITDYLCTASVYVNLISYDRYOSVNAV 120  
Db 61 DFFGVGISIPLYIPHTLFEWDFGKEICVFWLTTDYLCTASVYVNLISYDRYOSVNAV 120  
Qy 121 SYRAQTGIMKIQAQVAVMILAFVNGPMLASDSWKNTNTKDCBPGFVTEWYILTIT 180  
Db 121 SYRTQHTGVLKIVTLMAVAVLAFVNGPMLVSESMKDEGS--ECBPGFSEWYILAIT 178  
Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRALSRCPHAGFTSTSSASGHLRHAGVACTSN 240  
Db 179 SFLEFVPIVILVAYFNNIYWSLWKRLSRCSQHPGLTAVSSNICGHSFRGRSSRSL 238  
Qy 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSPWRSESAAALRQREYAEILRG 300  
Db 239 SASTEVPAFHSERQRRKSSLMFSRTYKMSNTIASKMGFSQSDSVALLHQREHVELLRA 298  
Qy 301 RKLARSLAILLSAFAICWAPYCLFTIIVLSTYPTPTERPKSVWYSIAFWLQWNSFVNPPLY 360  
Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPPLY 358  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390  
RESULT 6  
AAB62445  
ID AAB62445 standard; protein; 390 AA.  
XX AAB62445;  
XX  
DT 09-JUL-2001 (first entry)  
DE Human GPCR-like polypeptide, PFI-013.  
XX  
XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;  
KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;  
KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;  
KW signal transduction.  
XX Homo sapiens.  
XX EP1096009-A1.  
XX  
PD 02-MAY-2001.  
XX  
XX 24-OCT-2000; 2000EP-00309364.  
XX  
PR 29-OCT-1999; 99GB-00025641.  
PR 20-APR-2000; 2000GB-00009973.  
XX  
XX (PFI2 ) PFIZER LTD.  
PA (PFI2 ) PFIZER INC.  
XX  
XX Peter B, O'reilly MA;  
PI  
XX WPI; 2001-309854/33.  
DR N-PSDB; AAF83203.  
DR  
XX New G-protein coupled receptor-like polypeptide, polynucleotide for  
PT screening drug candidates for treating diseases associated with signal  
PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.  
XX  
XX Claim 22; Page 44; 66pp; English.  
XX  
XX This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-  
CC 013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed  
CC by standard recombinant methodology. Antibodies and modulators of PFI-013

CC are useful in the manufacture of a medicament for treating allergic  
CC disorder, including exstrinsic asthma, immunological disorders, such as  
CC intrinsic asthma, vasculitic granulomatous disease, interstitial and  
CC other pulmonary disease, including chronic obstructive pulmonary disease  
CC (COPD), infectious, inflammatory disease, such as inflammatory bowel  
CC disease and neoplastic and myeloproliferative diseases. They are also  
CC useful for treating obesity, diabetes, metabolic, neurological diseases,  
CC psychotherapeutics, urogenital disease, reproduction and sexual medicine,  
CC inflammation, cancer, tissue repair, dermatology, photoaging, skin  
CC pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases,  
CC allergy and respiratory disease, sensory organ disorders, sleep disorders  
CC and hair loss. The PFI-013 protein and nucleic acid are useful in the  
CC diagnosis and treatment of the above conditions and also for screening  
CC drug candidates for the treatment of diseases associated with signal  
CC transduction. The antibodies are also useful for enrichment of  
CC eosinophils from mammalian, especially human blood and for detecting the  
CC protein in biological samples  
XX Sequence 390 AA;  
SQ  
Query Match 66.9%; Score 1370.5; DB 4; Length 390;  
Best Local Similarity 68.1%; Pred. No. 6.5e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
Qy 1 MSENSTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNLRHSNYFFLNLAIS 60  
Db 1 MPDNTNINSLSTRVTLAFFMSLVAFAMLGNALVILAFVVDKLNLRHSNYFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPHLVFNNGSGICMFWMITDYLCTASVYVNLISYDRYOSVNAV 120  
Db 61 DFFGVGISIPLYIPHTLFEWDFGKEICVFWLTTDYLCTASVYVNLISYDRYOSVNAV 120  
Qy 121 SYRAQTGIMKIQAQVAVMILAFVNGPMLASDSWKNTNTKDCBPGFVTEWYILTIT 180  
Db 121 SYRTQHTGVLKIVTLMAVAVLAFVNGPMLVSESMKDEGS--ECBPGFSEWYILAIT 178  
Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRALSRCPHAGFTSTSSASGHLRHAGVACTSN 240  
Db 179 SFLEFVPIVILVAYFNNIYWSLWKRLSRCSQHPGLTAVSSNICGHSFRGRSSRSL 238  
Qy 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSPWRSESAAALRQREYAEILRG 300  
Db 239 SASTEVPAFHSERQRRKSSLMFSRTYKMSNTIASKMGFSQSDSVALLHQREHVELLRA 298  
Qy 301 RKLARSLAILLSAFAICWAPYCLFTIIVLSTYPTPTERPKSVWYSIAFWLQWNSFVNPPLY 360  
Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPPLY 358  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390  
RESULT 7  
AAG64477  
ID AAG64477 standard; protein; 390 AA.  
XX AAG64477;  
XX  
XX 25-SEP-2001 (first entry)  
DT  
XX Human G protein-coupled receptor protein BG26.  
DE  
XX Human; G protein-coupled receptor protein BG26; histamine H3; histamine;  
KW altering intracellular cAMP concentration;  
KW regulating signal transduction.  
XX  
XX Homo sapiens.  
XX WO200146414-A1.  
XX  
XX 28-JUN-2001.  
PD  
XX

```
PF 20-DEC-2000; 2000WO-JF009038.
XX
XX 20-DEC-1999; 99JP-00361687.
XX
XX (BANY ) BANYU PHARM CO LTD.
XX
XX Itadani H, Nakamura T, Tanaka K, Ohta M;
XX WPI; 2001-441675/47.
XX N-PSDB; AAH47911.
XX
XX G protein-coupled receptor protein BG26, with activity of binding to
XX histamine and capable of changing intracellular cAMP concentration in
XX response to its stimulus, applicable as tool in screening ligands or drug
XX candidates.
XX
XX Claim 1; Page 41-44; 50pp; Japanese.
XX
XX The present sequence is that of the human G protein-coupled receptor
XX protein BG26, which shows significant homology with histamine H3, with
XX activity of binding to histamine and capable of changing intracellular
XX cAMP concentration in response to its stimulus. The protein is applicable
XX as a tool in screening ligands or drug candidates for regulating signal
XX transduction from such protein and treating diseases associated with its
XX abnormality
XX
XX Sequence 390 AA;
XX
XX Query Match 66.9%; Score 1370.5; DB 4; Length 390;
XX Best Local Similarity 68.1%; Pred. No. 6.5e-133;
XX Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
XX
Qy 1 MSENSTGILPPAAQVPLAFMLSFAPAIWGNVAVILAFVVDENLHRNYSFFLNLAIS 60
Db 1 MPTNSTINLSLSTRTVLAFFMSLVAFIMLGNALVILAFVVDKMLHRSSYFFLNLAIS 60
Qy 61 DFLVGLISILPIYIPHLVFNFGSGICWFWLITDYLCTASVNVNVLISYDRYQSVSNV 120
Db 61 DFFVGVVISILPIYIPHTLFEWDFGKEICVFWLITDYLCTASVNVNVLISYDRYLSVSNV 120
Qy 121 SYRAQHTGIMKIWAQVAVVILAFVNGPMLASDSWKNSTNTKDCPPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVLMAVAVVILAFVNGPMLVSESWKDEGS--ECEPFGPFSEWYILAIT 178
Qy 181 MLLEFLPLVLSVAVFVVOIYWSLWKRALSRCPSHAGFTTSSASGHLHRAGVACFTSN 240
Db 179 SFLEFVPLVILVAVFVNNIYWSLWKRDHLRCQSHPGLTAVSSNICGHSFRGLSSRRSL 238
Qy 241 PGLKESAAHSSESPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILRG 300
Db 239 SASTEVPAFSESRQRKSSLMFSRTKMSNTTASKMGFSQSDSVALLQREHVELLRA 298
Qy 301 RKLARSAILLSAFAICWAPYCLFTTIVLSTYPTPTPKSVWYISAFWLQWPNFSPVNPFLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWPNFSPVNPFLY 358
Qy 361 PLCHRRRQKAFKWLCLVTWKPALSQ-NQSVSS 391
Db 359 PLCHKRFQKAFKLFICIKQPLPSQHSRVSS 390
XX
RESULT 8
AAB73622
ID AAB73622 standard; protein; 390 AA.
XX
XX AAB73622;
XX
XX 10-AUG-2001 (first entry)
XX
XX Human G protein-coupled receptor AXOR35.
XX
XX AXOR35; human; G protein-coupled receptor; 7TM receptor;
XX histamine H3 receptor homologue; infection; viral; bacterial; fungal;
XX
```

```
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW severe depression; bipolar disorder; dyskinesia; Parkinson's disease;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery.
XX
XX Homo sapiens.
XX
XX WO200133221-A1.
XX
XX 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029461.
XX
XX 02-NOV-1999; 99US-00431898.
XX 03-FEB-2000; 2000US-00497790.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;
XX Michalovich D, Morrow DM, Zhu Y;
XX
XX WPI; 2001-316464/33.
XX N-PSDB; AAH24007.
XX
XX Novel G-protein coupled receptor polypeptide and polynucleotide for
XX treating cancer, autoimmune, pulmonary, cardiovascular and neurological
XX disorders and for identifying modulators useful for treating asthma.
XX
XX Claim 1; Page 50-51; 54pp; English.
XX
XX The invention relates to the human G protein-coupled receptor AXOR35
XX (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
XX and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
XX transmembrane domains and is involved in signal transduction. AXOR35 has
XX homology and structural similarity with G protein-coupled receptors such
XX as the human histamine H3 receptor. The invention also relates to
XX expression vectors and host cells comprising AXOR35 DNA, to recombinant
XX expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
XX including bacterial, fungal, protozoal and viral infections, particularly
XX HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
XX diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
XX urinary retention; acute heart failure; hypotension; hypertension; angina
XX pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
XX psychotic and neurological disorders such as anxiety, schizophrenia,
XX manic depression, depression, delirium, dementia, and severe mental
XX retardation, and dyskinesias, such as Parkinson's disease, Huntington's
XX disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
XX nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
XX antibodies may be used in screening compounds for their ability to
XX modulate AXOR35 activity or expression. Such AXOR35 modulators are
XX particularly useful for treating asthma, and inhibiting or promoting the
XX function of lymphocytes, macrophages, eosinophils or neutrophils in
XX asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
XX useful for diagnosing or determining susceptibility of an individual to a
XX disease via the detection of abnormal levels of protein or mRNA, or via
XX the detection of mutations in the corresponding gene. AXOR35 proteins are
XX also useful for inducing an immunological response in a mammal against
XX the above diseases, and for antibody production. AXOR35 nucleotides are
XX also useful as diagnostic reagents, in chromosome localisation and tissue
XX expression studies, and for producing transgenic animals useful in drug
XX discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
XX protein or fragments thereof, and are also useful for treating conditions
XX associated with the expression of the AXOR35 protein. The present
XX sequence represents human AXOR35
```



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XX      Sequence 390 AA;
SQ      Query Match
      Best Local Similarity 66.9%; Score 1370.5; DB 4; Length 390;
      Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy      1 MSENSTGILPPAAQVPLAFIMSSFAFIMVGNVAVILAFVVDRLNLRHSRYFFLNLAIS 60
Db      1 MPDNTSTINLSLSTRVTTLAFPMSLVAFALMGLNALVILAFVVDKLNLRHSRYFFLNLAIS 60

Qy      61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYINVLISYDRYOSVSNV 120
Db      61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYINVLISYDRYLSVSNV 120

Qy      121 SYRAQHTGIMKIVAQMWILAFVLNGPMLIASDSWKNSTNTKDCFPFVTEWYILIT 180
Db      121 SYRTQHTGVKIVLWVAVVLAFVLNGPMLIVSESMKDEGS--ECEPGFFSEWYILAIT 178

Qy      191 MLLFLLPVIISVAPNVOIYWSLWKRRALSRCPHAGSTTSSASGHLHRAGVACRTSN 240
Db      179 SFLEFVIVPILVAVFNNMIYWSLWKRRDLRCSRQSHPGLTAVSSNICGHSFRGLSSRSL 238

Qy      241 PGLKESARSRSESPRRKSSILVSLRTHMNSITAFKVGSPWRSFSAALROREYAEILRG 300
Db      239 SASTEVPAFSHSEQRQRKSSLMFSRRTKNSNTTASRKGSPSQSDSVLHQREHVELLRA 298

Qy      301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSYAFWLQWNSFVNPLY 360
Db      299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRTAFWLQWNSFVNPLY 358

Qy      361 PLCHRRFOKAFKWLICVTWKPALSQ--NOSVSS 391
Db      359 PLCHKRFQAFKLFKICIKKQLPSQHSRSVSS 390

RESULT 9
AAM53050
ID      AAM53050 standard; protein; 390 AA.
AC
XX
XX      AAM53050;
XX
XX      26-MAR-2002 (first entry)
XX
XX      Human G protein-coupled receptor nGPCR-2067.
XX
KW      Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor;
KW      signal transduction; mental disorder; central nervous system disease;
KW      metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;
KW      psychotic disorder; Huntington's disease; schizophrenia; migraine;
KW      depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;
KW      Parkinson's disease; proliferative disorder; cancer; psoriasis;
KW      benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia;
KW      thyroid disorder; cardiovascular disease; hypotension; hypertension;
KW      thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;
KW      inflammatory conditions; autoimmune disorder; rheumatoid arthritis;
KW      hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;
KW      antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic;
KW      cardiant; antiatherosclerotic; neuroleptic; antimigraine;
KW      antiparkinsonian; tranquiliser; antidepressant; neuroprotective;
KW      anticonvulsant; antiinflammatory; antirheumatic; antiarthritic;
KW      antipsoriatic; gene therapy; receptor.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Domain
FT      Location/Qualifiers
FT      19..41
FT      /label= Transmembrane_domain_1
FT      52..74
FT      /label= Transmembrane_domain_2
FT      86..110
FT      /label= Transmembrane_domain_3
FT      128..146
FT      /label= Transmembrane_domain_4
FT      172..194
FT      /label= Transmembrane_domain_5
FT      305..326
FT      /label= Transmembrane_domain_6
FT      342..360
FT      /label= Transmembrane_domain_7
XX      WO200185793-A2.
XX      15-NOV-2001.
XX      08-MAY-2001; 2001WO-US014750.
XX      08-MAY-2000; 2000US-0203108P.
XX      (PHAA ) PHARMACIA & UPJOHN CO.
XX      Lind P, Sejltitz T, Vogeli G, Wood LS;
XX      WPI; 2002-062240/08.
XX      N-PSDB; ABA02496.
XX      New polynucleotide, useful for identifying modulator compounds which are
XX      used for treating psoriasis, schizophrenia, diabetes, encodes the novel G
XX      protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).
XX      Claim 31; Page 63; 100pp; English.
XX
XX      This sequence represents a novel human G protein-coupled receptor (GPCR)
XX      designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative
XX      transmembrane domains and is involved in signal transduction. The
XX      invention also relates to expression vectors and host cells comprising
XX      nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-
XX      2067, to antibodies specific for nGPCR-2067, to drug screening methods
XX      that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067
XX      nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants
XX      and species homologues and may also be used in genetic mapping. The
XX      invention also discloses the use of nGPCR-2067 nucleic acids in screening
XX      for a predisposition to nGPCR-2067-associated hereditary mental
XX      disorders, or for the diagnosis of these disorders. nGPCR-2067 nucleic
XX      acids may additionally be used to generate transgenic animals, including
XX      knockout animals, which may provide an insight into treating a variety of
XX      human disorders, and may also be used in the design of antisense
XX      molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067,
XX      and nGPCR-2067 modulators may be used to treat a wide variety of medical
XX      conditions, particularly mental disorders. Diseases that may be treated include
XX      diseases, and metabolic diseases. Diseases that may be treated include
XX      viral infections, particularly HIV-1 or HIV-2 infections; pain; central
XX      nervous system, neurological and psychotic disorders such as Huntington's
XX      disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,
XX      dementia, Alzheimer's disease, and Parkinson's disease; proliferative
XX      disorders such as cancers, benign prostatic hypertrophy and psoriasis;
XX      metabolic disorders such as diabetes, dyslipidaemia, obesity, and
XX      anorexia; thyroid disorders; cardiovascular diseases such as hypotension,
XX      hypertension, thrombosis, myocardial infarction, cardiomyopathies, and
XX      atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,
XX      rheumatoid arthritis); hormonal disorders; and renal failure
XX
SQ      Sequence 390 AA;
      Query Match
      Best Local Similarity 66.1%; Score 1370.5; DB 5; Length 390;
      Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy      1 MSENSTGILPPAAQVPLAFIMSSFAFIMVGNVAVILAFVVDRLNLRHSRYFFLNLAIS 60
Db      1 MPDNTSTINLSLSTRVTTLAFPMSLVAFALMGLNALVILAFVVDKLNLRHSRYFFLNLAIS 60

Qy      61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYINVLISYDRYOSVSNV 120
Db      61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYINVLISYDRYLSVSNV 120

```



XX Behan JX, Hedrick JA, Laz TW, Monsma FJ, Morse KL, Umland SP;  
PI Wang S;

XX WPI; 2002-673827/72.

XX N-PSDB; ABW78739.

XX Novel mammalian histamine receptor polypeptide useful for identifying  
PT agonist or antagonist for treating diseases such as inflammation, asthma,  
PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.

XX Claim 2; Page 16-17; 21pp; English.

XX The present sequence represents a histamine receptor. The polypeptide is  
CC useful for identifying an agonist or antagonist of a mammalian histamine  
CC receptor. It is useful as an antigen to elicit the production of  
CC antibodies. The histamine receptor polypeptide and polynucleotide are  
CC useful in the treatment and management of diseases such as inflammation,  
CC asthma, allergy, atopic dermatitis, stroke, myocardial infection,  
CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid  
CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.  
CC They are also useful for modulating intracellular second messenger  
CC pathway activated through histamine receptors (cyclic-AMP, calcium,  
CC inositol phosphate and mitogen activated protein (MAP) kinase), changes  
CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca<sup>2+</sup>  
CC mobilization, mitogenic effects, etc

XX Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;

Best Local Similarity 68.1%; Pred. No. 6.5e-133;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMLSSFAFIMVGNVILAFVVDRLNHRNSYFFLNLAIS 60

DB 1 MPDTNSTINLSLSTRTVLAFMSLVAFIMLGNALVILAFVVDKLNHRSSYFFLNLAIS 60

QY 61 DFLVGLISILPIYIPHLFNNFGSGICMFWLITDYLCTASVYVNIIVLISYDRYQSVNAV 120

DB 61 DFFVGVISILPIYIPHTLFEWDFGKEICVFWLITDYLCTASVYVNIIVLISYDRYQSVNAV 120

QY 121 SYRAQHTGIMKIIVAQVAVVILAFVNGPMLASDSWKNSNTNKDCBPGFVTEWYILIT 180

DB 121 SYRTQHTGVILKIVTLVAVVILAFVNGPMLVSESWKDEGS--ECEPGFSEWYILAIT 178

QY 181 MLLEFLLPVTSVAYFNVQIYWSLWKRRALSRCPHAGFTTSSASGHLHRAGVACRTSN 240

DB 179 SFLEFVIPVILVAYFNNIYWSLWKRDHLRCQSHPGLTAVSSNICGHSFRGLSSRRSL 238

QY 241 PGLKESAAHRSHSPRRKSSILVSLRTHMNSSITAFKVGFWSESAALRQREYAEILRG 300

DB 239 SASTEVPAFPHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLHQREHVELLA 298

QY 301 RKLARSLAILLAPAIQWAPYCLFTIVLSTYPTPRTERPKSVWYISAFWLQFNFSVNPFLY 360

DB 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVWYIRAFWLQFNFSVNPFLY 358

QY 361 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 391

DB 359 PLCHRRFQKAFKILCFIKQPLPSQHSRVSS 390

RESULT 12

AAM50564

ID AAM50564 standard; protein; 390 AA.

XX AAM50564;

XX 18-MAR-2002 (first entry)

XX Human histamine H4 receptor.

XX Histamine H4 receptor; human; antiasthmatic; antiallergenic;

KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.

OS Homo sapiens.

PN W0200192485-A1.

XX 06-DEC-2001.

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WPI; 2002-114339/15.

XX N-PSDB; AAI70980.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding

PT the proteins, useful in gene therapy for treating diseases where it is

PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 13; Fig 2; 92pp; English.

XX The present sequence is that of a human histamine receptor of the H4  
CC subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA  
CC library. The invention provides mammalian (human, mouse, rat and guinea  
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the human histamine H4 receptor. Such modulators may be  
CC useful for diagnosing, treating or preventing asthma, allergy,  
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
CC disorders of the neuroendocrine system, stress and spasticity

SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;

Best Local Similarity 68.1%; Pred. No. 6.5e-133;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMLSSFAFIMVGNVILAFVVDRLNHRNSYFFLNLAIS 60

DB 1 MPDTNSTINLSLSTRTVLAFMSLVAFIMLGNALVILAFVVDKLNHRSSYFFLNLAIS 60

QY 61 DFLVGLISILPIYIPHLFNNFGSGICMFWLITDYLCTASVYVNIIVLISYDRYQSVNAV 120

DB 61 DFFVGVISILPIYIPHTLFEWDFGKEICVFWLITDYLCTASVYVNIIVLISYDRYQSVNAV 120

QY 121 SYRAQHTGIMKIIVAQVAVVILAFVNGPMLASDSWKNSNTNKDCBPGFVTEWYILIT 180

DB 121 SYRTQHTGVILKIVTLVAVVILAFVNGPMLVSESWKDEGS--ECEPGFSEWYILAIT 178

QY 181 MLLEFLLPVTSVAYFNVQIYWSLWKRRALSRCPHAGFTTSSASGHLHRAGVACRTSN 240

DB 179 SFLEFVIPVILVAYFNNIYWSLWKRDHLRCQSHPGLTAVSSNICGHSFRGLSSRRSL 238

QY 241 PGLKESAAHRSHSPRRKSSILVSLRTHMNSSITAFKVGFWSESAALRQREYAEILRG 300

DB 239 SASTEVPAFPHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLHQREHVELLA 298

QY 301 RKLARSLAILLAPAIQWAPYCLFTIVLSTYPTPRTERPKSVWYISAFWLQFNFSVNPFLY 360

DB 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVWYIRAFWLQFNFSVNPFLY 358

QY 361 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 391

||||:||||| |||:| | | | | :|||  
 359 PLCHRFQKAFKIFCIKKQPLPSQHSRSVSS 390

## RESULT 13

AAAG66023  
 ID AAG66023 standard; protein; 390 AA.

XX AC AAG66023;

XX DT 27-FEB-2002 (first entry)

XX DE Human histamine H4 receptor protein.

XX KW Histamine receptor; H4; anti-rheumatic; antiarthritic; immunosuppressive;  
 KW antiallergic; neuroprotective; antidiabetic; human;  
 KW cerebroprotective; cAMP modulator; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Domain 12..40  
 FT /note= "transmembrane domain"  
 FT Domain 52..69  
 FT /note= "transmembrane domain"  
 FT Domain 88..110  
 FT /note= "transmembrane domain"  
 FT Domain 130..154  
 FT /note= "transmembrane domain"  
 FT Domain 172..196  
 FT /note= "transmembrane domain"  
 FT Domain 304..325  
 FT /note= "transmembrane domain"  
 FT Domain 342..362  
 FT /note= "transmembrane domain"

XX WO200185786-A2.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US014527.

XX 05-MAY-2000; 2000US-0202151P.

XX 23-AUG-2000; 2000US-0227567P.

XX 13-NOV-2000; 2000US-0247855P.

XX (AMHP ) AMERICAN HOME PROD CORP.

XX Jones PG, Blatcher M, Wu S, Pausch MH;

XX WPI; 2002-049442/06.

XX N-PSDB; AAI67750.

XX New histamine receptor, termed H4 useful for detecting H4 (ant)agonists  
 for treating transplanted organ rejection, asthma, allergy, multiple  
 sclerosis and rheumatoid arthritis.

XX Claim 5; Fig 1; 66pp; English.

XX The invention provides an isolated histamine receptor, H4, which binds  
 ligands comprising imidazole attached to amine by an alkyl chain. The H4  
 receptor can be expressed by standard recombinant methodology. Cells  
 expressing H4 receptor protein at a detectable level can suppress cyclic  
 adenosine monophosphate (cAMP) formation when contacted with the H4  
 receptor agonist. The H4 receptor and antibodies are used for identifying  
 H4 receptor modulators. Modulation of histamine H4 receptors is useful  
 for treating transplanted organ rejection, asthma, allergies and  
 autoimmune pathologies such as multiple sclerosis, type I diabetes,  
 rheumatoid arthritis, cognitive and memory defects. The H4 receptor  
 protein and nucleic acids are useful targets to identify drugs that are  
 effective in treating disorders associated with histamine-regulated  
 processes. Identification and isolation of H4 receptor provides for  
 development of screening of molecules that interact with H4 receptors.

CC Genetic variants of H4 can be used to diagnose an H4 associated disease  
 as described above. The H4 receptor polynucleotide is useful to treat or  
 CC prevent a disorder associated with the function of H4 in peripheral blood  
 CC leukocytes. The present sequence represents the human histamine H4  
 CC receptor protein

XX SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;

Best Local Similarity 68.1%; Pred. No. 6.5e-133;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMLSSFAFMVGNVAVILAFVVDNRNLRHRSNYFFLNLAIS 60

DB 1 MPDTNSTINLSLSTRVTLAFPMSLVAFIMLGNALVILAFVVDKRLRHSRYFFLNLAIS 60

QY 61 DFVUGLISPLYIPHYLFWNFSGICMFWLITDYLLCTASVYNIYLISYDRYQSVSNV 120

DB 61 DFFVGVISPLYIPTLFEWDFGKEICVFWLITDYLLCTASVYNIYLISYDRYLSVSNV 120

QY 121 SYRAQHTGIMKIVAQVAVVAVILAFVNGPMILASDSKNSNTNTKDCPFGFVTEWYILTIT 180

DB 121 SYRTQHTGVLLKIVTLVAVVAVVILAFVNGPMILVSEKWDGEGS--ECPFGFSEWYILAIT 178

QY 181 MLLEFLLPVISVAYFNQIYVSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACTSN 240

DB 179 SFLEFVIPVLVAYFNQIYVSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACTSN 238

QY 241 PGLKESAAASHSESPPKSSILVSLRTHMSSITAFKVSFWSESNAALQREVAELLRG 300

DB 239 SASTEVPASPHSRQRKSLMFSRTKMSNTIASKMGFSQSDSVVALHQREHVELLRA 298

QY 301 RKLARSLAILLSAFAICWAPYCLTIVLSTYPRTERPKSVWYISIAFWLQNFNSFVNPFY 360

DB 299 RRLAKSLAILLGVFVAVCWAPYSLTIVLSFYSSATGPKSVWYRIAFWLQNFNSFVNPFY 358

QY 361 PLCHRFQKAFKILCVTKWPALSQ-NQSVSS 391

DB 359 PLCHRFQKAFKIFCIKKQPLPSQHSRSVSS 390

## RESULT 14

AAU74906

ID AAU74906 standard; protein; 390 AA.

XX AC AAU74906;

XX DT 09-APR-2002 (first entry)

XX DE Amino acid sequence of human G-protein coupled receptor TGR62 protein.

XX KW Human; G-protein coupled; receptor; GPCR; TGR62; kidney disease;

XX KW signal transduction modulator; cerebral cavernous malformation;

XX KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;

XX KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;

XX KW spleen-associated disorder; immune disorder.

XX OS Homo sapiens.

XX FN WO200200719-A2.

XX PD 03-JAN-2002.

XX PF 25-JUN-2001; 2001WO-US020363.

XX PR 23-JUN-2000; 2000US-0213461P.

XX PA (TULA-) TULARIK INC.

XX PI Lin DC, Zhao J, Chen J, Cutler G;

XX WPI; 2002-147880/19.

XX DR N-PSDB; ABK12959.

XX New G-protein coupled receptor polypeptides, useful for identifying  
PT modulators of signal transduction for treating kidney disease,  
PT hyperlipidemia, obesity, dyslexia and cardiac myxoma.  
XX  
PS Claim 26; Page 61; 78pp; English.  
XX  
CC The present invention relates to a new G-protein coupled receptor (GPCR)  
CC polypeptide comprising greater than 70% amino acid sequence identity to  
CC the amino acid sequence of human GPCRs TGR2, TGR130.1, TGR130.2,  
CC human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or  
CC 90% amino acid sequence identity to human novel edg receptor protein, as  
CC defined in the specification. The GPCR covalently linked to a solid phase  
CC is useful for identifying a compound that modulates signal transduction.  
CC The identified compounds are useful for treating kidney disease, cerebral  
CC cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac  
CC myxoma. The molecules of the invention are useful for diagnosing  
CC disorders or conditions such as kidney-related conditions or diseases  
CC such as renal failure, nephritis, nephrotic syndrome, asymptomatic  
CC urinary abnormalities, renal tubule defects, hypertension and  
CC nephrolithiasis, liver-related disease or condition e.g. cirrhosis,  
CC infiltrations, lesions, functional disorders and jaundice and spleen-  
CC associated disorders or conditions e.g. splenic enlargement, immune  
CC disorders, blood disorders and others. Modulation of the polypeptide of  
CC the invention is useful to treat or prevent any of the above conditions  
CC or diseases. The present amino acid sequence represents the human GPCR  
CC TGR62 protein of the invention. This sequence is one of seven novel G  
CC protein coupled receptors of the invention (AAU74904- AAU74911)  
XX  
SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
Best Local Similarity 68.1%; Pred. No. 6.5e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
Qy 1 MSENSTGILPPAAQVPLAFMSFAIMVGNVILAFVVDNLRHRSYFFNLAI 60  
Db 1 MPDNTNINSLSTRVTLAFPMSLVAFIMLGNALVILAFVVDNLRHRSYFFNLAI 60

Qy 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYNIIVLSYDRYOSVNAV 120  
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTYLLCTASVYNIIVLSYDRYUSNAV 120  
Qy 121 SYRAQHTGIMKIVAOVMVILAFVNGPMLASDKNSNTKDCBPGFVTEWYILIT 180  
Db 121 SYRTQHTGVLKIVTLWAVVILAFVNGPMLIVSESMKDEGS--ECEPGFSEWYILAIT 178  
Qy 181 MLLEFLIPVIVAVFNQIYWSLWKRLSRCPSHAGFTTSSASGHLHRAGVACTSN 240  
Db 179 SFLEFVIVPILVAYFNNNIYWSLWKRDHLRCQSHGLTAVSSNICGHSFRGLSSRRSL 238  
Qy 241 PGLKESAAHRSSEPRKSSITLVSLRTHMNSSITAFKVGSPWRSSEALRQREYAEILRG 300  
Db 239 SASTEVPAFSEHQRKRSKLSMFSSRTNMSNTTASKMGFSQSDSVLHQREHVELLR 298  
Qy 301 RKLARSAILLSAPACWAPYCLFTIIVLSTYPRTERPKSVWYISAFWLQFNFSVPNPLY 360  
Db 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVWYIRAFWLQFNFSVPNPLY 358  
Qy 361 PLCHRRFQKAFWKILCVTKWPAISQ-NQSVSS 391  
Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRVSS 390

RESULT 15  
ABG71960  
ID ABG71960 standard; protein; 390 AA.  
XX  
AC ABG71960;  
XX  
DT 28-JAN-2003 (first entry)  
XX  
DE Human G-protein coupled receptor AXOR35.

XX Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte;  
KW macrophage; eosinophil; neutrophil; infection; transplant rejection;  
KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
KW psoriasis; urological disease; urinary retention; cardiovascular disease;  
KW myocardial infarction; hypotension; hypertension; pulmonary disorder;  
KW chronic obstructive pulmonary disease; cough; renal disease;  
KW renal ischaemia; arteriosclerosis; atherosclerosis; psychosis;  
KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;  
KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;  
KW graft versus host disease; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
PN US2002137054-A1.  
XX  
PD 26-SEP-2002.  
XX  
XX 20-JUL-2001; 2001US-00910411.  
XX  
XX 02-NOV-1999; 99US-00431898.  
XX  
XX 03-FEB-2000; 2000US-00497790.  
XX  
XX 20-OCT-2000; 2000US-00693761.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX Aubart KM, Bergsma DJ, Fitzgerald L, Graybill TL, Li X;  
XX Michalovich D, Morrow DM, Zhu Y;  
XX WPI; 2003-074982/07.  
XX  
XX N-PSDB; ABS57063.  
XX  
XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for  
XX treating infections, gastrointestinal disorders, autoimmune disorders,  
XX urological diseases, cardiovascular diseases and cancer.  
XX  
XX Claim 1; Page 22; 24pp; English.

The invention relates to an isolated G-protein coupled receptor polypeptide, AXOR35, (and its homologues and variants) and its encoding polynucleotide (and its homologues, variants, complements and RNA equivalents). Also included are an anti-AXOR35 antibody, an AXOR35 expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell produces AXOR35, a membrane of the host cell expressing AXOR35, identifying/screening for agonists or antagonists of AXOR35 and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 agonists or antagonists. The agonist or antagonist identified is useful for treating a disease such as asthma, or for inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue such as an asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays, for identifying compounds that are agonists or antagonists of AXOR35, as vaccines, or for treating infections (bacterial, fungal, protozoan or viral infections), transplant rejection, gastrointestinal disorders (such as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease), irritable bowel syndrome, vomiting, inflammation (such as atopic dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis, psoriasis), urological diseases (such as urinary retention), cardiovascular diseases (such as myocardial infarction), hypotension, hypertension, pulmonary disorders (such as chronic obstructive pulmonary disease), cough, renal diseases (such as renal ischaemia), arteriosclerosis, atherosclerosis, psychotic and neurological disorders (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such as Parkinson's disease), cancer, obesity, stroke, septic shock, graft versus host disease and osteoporosis. The present sequence represents human AXOR35

Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 6; Length 390;  
Best Local Similarity 68.1%; Pred. No. 6.5e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSESNTGILPPAAQVPLAFIMSGFAFAMVGNVILAFVVDRLNRHRSNYFPFLNLAIS 60  
|::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
Db 1 MPDNTNINLSLSTRVTLAFMSLVAFAMLGNALVILAFVVDKRLRHRSSYFFFLNLAIS 60

Qy 61 DFLVGLISIDPLYIPHLFNNFSGICMFWLTIDYLLCTASVYNIVLISYDRYQSUSNAV 120  
||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
Db 61 DFFVGVISIDPLYIPHTLFEDWDFGKEICVFWLTIDYLLCTASVYNIVLISYDRYLSVNAV 120

Qy 121 SYRAQHTGIMKIVAQMVAVVILAFVNGPMLASDSWKNSTNTKDCPEPGFVTEWYIILIT 180  
||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
Db 121 SYRTQHTGVULKIVTLMAVVVILAFVNGPMLLYSESWKDEGS--ECEPGFSEWYILAIT 178

Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACRTSN 240  
|||::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
Db 179 SFLEFVIPVILVAYFNNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFGRLLSRRSL 238

Qy 241 PGLKESASRSHSESPREKSTILYSLRTHMNSSITAFKVGSWFWSSESALRQREYAEILRG 300  
||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKMNSNTIASKQGSFOSDSVALHQRBHVELLRA 298

Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYISIAFWLQWNSFVNPFLY 360  
|::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
Db 299 RRLAKSLAILLGVFAVCWAPYSLETTIVLSFYSSATGPKSVWYRIAFAFWLQWNSFVNPFLY 358

Qy 361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391  
|||::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||  
Db 359 PLCHRRFQKAFWKILCFIKKQPLPSQHSRSVSS 390

Search completed: May 24, 2006, 13:40:59  
Job time : 198 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 24, 2006, 13:32:11 ; Search time 25 Seconds  
(without alignments)  
1504.830 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
Sequence: 1 MSSNSTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1370.5	66.9	390	2 JC7566	histamine H4 recep
2	413	20.2	460	2 S09508	muscarinic acetyl
3	413	20.2	460	2 A24325	muscarinic acetyl
4	410.5	20.0	531	2 JT0531	muscarinic acetyl
5	410.5	20.0	590	2 S01114	muscarinic acetyl
6	410	20.0	460	2 I51837	muscarinic recept
7	410	20.0	460	2 A29514	muscarinic acetyl
8	409.5	20.0	590	2 S47572	muscarinic acetyl
9	403	19.7	589	2 A29476	muscarinic acetyl
10	402.5	19.7	590	2 S10128	muscarinic acetyl
11	402	19.6	589	2 B29514	muscarinic acetyl
12	401	19.6	639	2 A55019	muscarinic acetyl
13	400	19.5	460	2 A31897	muscarinic acetyl
14	399.5	19.5	532	2 JT0530	muscarinic acetyl
15	392.5	19.2	477	2 S71323	alpha-1A adrenergi
16	392	19.1	490	2 A35546	muscarinic acetyl
17	390.5	19.1	400	2 G00013	D3 dopamine recept
18	390.5	19.1	501	2 JH0447	alpha-1A-adrenergi
19	389.5	19.0	400	2 G01977	d3 dopamine recept
20	389.5	19.0	515	2 A40491	alpha-1-adrenergi
21	388.5	19.0	491	2 A41632	histamine H1 recep
22	388.5	19.0	572	2 I39369	alpha-1A-adrenergi
23	386.5	18.9	487	2 JC2495	histamine H1 recep
24	385.5	18.8	488	2 I56507	histamine H1 recep
25	384.5	18.8	517	2 A45121	alpha-1B adrenergi
26	382.5	18.7	560	2 A38731	alpha-1A adrenergi
27	382	18.7	479	2 S10127	muscarinic acetyl
28	380.5	18.6	466	2 S10126	muscarinic acetyl
29	380.5	18.6	501	2 T18863	hypothetical prote

30 380 18.6 432 2 I50829  
31 380 18.6 466 2 A40972  
32 379.5 18.5 466 2 JH0197  
33 379.5 18.5 466 2 S10856  
34 379.5 18.5 515 2 JC1525  
35 379 18.5 486 2 JC1415  
36 379 18.5 486 2 JC1415  
37 376 18.4 478 2 C29514  
38 374.5 18.3 479 2 S33776  
39 369.5 18.0 466 2 A27386  
40 367.5 17.9 366 2 A47321  
41 367 17.9 484 2 S48657  
42 366.5 17.9 484 2 S58868  
43 366 17.9 466 2 A35375  
44 364.5 17.8 366 2 A47385  
45 360.5 17.6 366 2 S26048

ALIGNMENTS

RESULT 1

JC7566  
histamine H4 receptor, HH4R - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: JC7566  
R;Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.  
Biochem. Biophys. Res. Commun. 279, 615-620, 2000  
A;Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.  
A;Reference number: JC7566; MUID: 20568725; PMID:11118334  
A;Contents: Leukocyte  
A;Accession: JC7566  
A;Molecule type: mRNA  
A;Residues: 1-390 <NAK>  
A;Cross-references: UNIPROT:Q9H3N8; UNIPARC:UPI0000039A92; DBBJ:AB045370  
C;Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled  
C;Genetics:  
A;Gene: hh4r  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 66.9%; Score 1370.5; DB 2; Length 390;  
Best Local Similarity 68.1%; Pred. No. 1.4e-111;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
Qy 1 MSSNSTGILPPAAQVPLAFIMSGSAFAIMVGNAAVILAFVVDRLNRHRSYFFLNLAIS 60  
Db 1 MPDINSTINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDKXLRHRSYFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPIHVLFPNNFGSGICMFWLITDYLICTASVYVNIIVLISYDRYQSVSNV 120  
Db 61 DFFVGVISIPLYIPTLFEWDFGKEICVFWLITDYLICTASVYVNIIVLISYDRYLSVSNV 120  
Qy 121 SYRAQHTGIMKIIVAQVAVVILAFVNGPMLASDSWKNSTNTKCPGFFVTEWVILIT 180  
Db 121 SYRTQHTGVLUKIIVLAVVAVVILAFVNGPMLILVSESWKDEGS--ECPGFFSEWVILAIT 178  
Qy 181 MLLEFLPVISVAYFNVQIYVSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240  
Db 179 SFLEFVIPVILVAYFNNIYVSLWKRDHLSRQCQSHGLTAVSSNICGHSFGRLLSSRRSL 238  
Qy 241 PGLKESAAHSRSHSSPRKSSILVSLRTHMSSITAFKVGSPWRSESALRQREVAELLRG 300  
Db 239 SASTEVPASPHSERQRRKSSLMFSSRTKMSNTIASXMGSPSQSDSVALHQREVELLRA 298  
Qy 301 RKLARSIALILSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFNPNPLY 360  
Db 299 RLRAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIRAFWLQWNSFNPNPLY 358  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391  
Db 359 PLCHRRFQKAFKILFCIKKQPLPSQHSRSVSS 390

## RESULT 2

S09508  
muscarinic acetylcholine receptor M1 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S09508; S06327; S04326  
R;Chapman, C.G.; Browne, M.J.  
Nucleic Acids Res. 18, 2191, 1990  
A;Title: Isolation of the human m1 (Hml) muscarinic acetylcholine receptor gene by PCR  
A;Reference number: S09508  
A;Accession: S09508  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-460 <CHA>  
A;Cross-references: UNIPROT:P11229; UNIPARC:UPI00001252AB; EMBL:X52068; NID:G34450; PIDN: A24325  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990  
R;Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.  
Nucleic Acids Res. 15, 10604, 1987  
A;Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.  
A;Reference number: S06327; MUID:90245684; PMID:2336407  
A;Accession: S06327  
A;Molecule type: DNA  
A;Residues: 1-460 <ALL>  
A;Cross-references: UNIPARC:UPI00001252AB; GB:X00508; NID:G297405; PIDN:CAA68  
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramchandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of two human muscarinic acetylcholine receptor subtypes.  
A;Reference number: S04326; MUID:88166632; PMID:3443095  
A;Accession: S04326  
A;Molecule type: DNA  
A;Residues: 1-172, 'M', 174-460 <PER>  
A;Cross-references: UNIPARC:UPI000005040F; EMBL:X15263; NID:G32317; PIDN:CAA33334.1; PIDN: A24325  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-kinase; G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-kinase  
F;25-50/Domain: transmembrane #status predicted <TM1>  
F;62-93/Domain: transmembrane #status predicted <TM2>  
F;100-121/Domain: transmembrane #status predicted <TM3>  
F;142-168/Domain: transmembrane #status predicted <TM4>  
F;187-209/Domain: transmembrane #status predicted <TM5>  
F;367-387/Domain: transmembrane #status predicted <TM6>  
F;402-420/Domain: transmembrane #status predicted <TM7>  
F;2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.28; Score 413; DB 2; Length 460;  
Best Local Similarity 27.48; Pred. No. 3.7e-28;  
Matches 122; Conservative 84; Mismatches 150; Indels 90; Gaps 19;  
QY 5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNVAVILAFVVDNRLHRSNYFFFLNLAISD 61  
DB 12 NITVLPAGKGPQVAFIGITITGLLSLATVGNLLVLSFKVNTLKTNNYFLLSLACAD 71  
QY 62 FLVGLISIPILYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120  
DB 72 LIIGTFSMNLYTYLLMGHWALGTACDLWLALDYVNASVNMNLLISFDYFSVTRPL 131  
QY 121 SYRAQHTGIMKIVAQMVAW-VILAFVNGPMILASDSWKNTK-----DCEPGFVTEW 174  
DB 132 SYRAKRT--PRRAALMIGLAWLSFVLWAPAIL---FWQYLVGERTVLAGOCYIQFLSQP 186  
QY 175 YILITITMLLEFLLPVISVAVFNQIVYWSLWKR-----RAL-----SRCPSHAGSTSSS 224  
DB 187 IIFGTAMAAFLPVTVMC-----TLYWRIYRETNRRARELAALQSGTTPGKGGSSSSSE 242  
QY 225 AS-----GHLHRAGVACRT-----RTHMNSSITAFKVGFWRSESA-----ALOREY 294  
DB 243 RSQPGAGSGPETPPGRCR---CCRAPRLLOAYSWKEEEDSGMESLTSSEGEPP--G 297  
QY 259 SSILVSL-----RTHMNSSITAFKVGFWRSESA-----ALOREY 294  
DB 298 SEVVIPKMPVDPEAQAPKQPPRSSPNTVKRPTKGRERAGKQKPRGKQOLAKRKT 354  
QY 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSF 354

DB 355 FSLVKEKKAARTLSAILLAPILTWTPYNIWMLV-STFKDCVPETLW-ELGYWLCYVNST 412

QY 355 VNPFLYPLCHRRRFQKAFWKILCVTKW 380

DB 413 INPMCALCNKAFRDTF-RLLLLCRW 437

## RESULT 3

A24325  
muscarinic acetylcholine receptor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 09-Jul-2004  
C;Accession: A24325  
R;Kubo, T.; Fukuda, K.; Mikami, A.; Maeda, A.; Takahashi, H.; Mishina, M.; Haga, T.; Hara, Y.  
Nature 323, 411-416, 1986  
A;Title: Cloning, sequencing and expression of complementary DNA encoding the muscarinic acetylcholine receptor.  
A;Reference number: A24325; MUID:87014801; PMID:3762692  
A;Accession: A24325  
A;Molecule type: mRNA  
A;Residues: 1-460 <KUB>  
A;Cross-references: UNIPROT:P04761; UNIPARC:UPI00001252AD; GB:X04413; NID:G1863; PIDN: A24325  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-kinase; G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-kinase  
F;25-50/Domain: transmembrane #status predicted <TM1>  
F;62-93/Domain: transmembrane #status predicted <TM2>  
F;100-121/Domain: transmembrane #status predicted <TM3>  
F;142-168/Domain: transmembrane #status predicted <TM4>  
F;187-209/Domain: transmembrane #status predicted <TM5>  
F;367-387/Domain: transmembrane #status predicted <TM6>  
F;402-420/Domain: transmembrane #status predicted <TM7>

Query Match 20.28; Score 413; DB 2; Length 460;  
Best Local Similarity 27.53; Pred. No. 3.7e-28;  
Matches 122; Conservative 83; Mismatches 154; Indels 84; Gaps 18;

QY 5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNVAVILAFVVDNRLHRSNYFFFLNLAISD 61

DB 12 NITVLPAGKGPQVAFIGITITGLLSLATVGNLLVLSFKVNTLKTNNYFLLSLACAD 71

QY 62 FLVGLISIPILYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120

DB 72 LIIGTFSMNLYTYLLMGHWALGTACDLWLALDYVNASVNMNLLISFDYFSVTRPL 131

QY 121 SYRAQHTGIMKIVAQMVAW-VILAFVNGPMILASDSWKNTK-----DCEPGFVTEW 174

DB 132 SYRAKRT--PRRAALMIGLAWLSFVLWAPAIL---FWQYLVGERTVLAGOCYIQFLSQP 186

QY 175 YILITITMLLEFLLPVISVAVFNQIVYWSLWKR-----RAL-----SRCPSHAGSTSSS 224

DB 187 IIFGTAMAAFLPVTVMC-----TLYWRIYRETNRRARELAALQSGTTPGKGGSSSSSE 242

QY 225 AS-----GHLHRAGVACRT-----RTHMNSSITAFKVGFWRSESA-----ALOREY 297

DB 243 RSQPGAGSGPETPPGRCR---CCRAPRLLOAYSWKEEEDSGMESLTSSEGEPP--G 297

QY 259 SSILVSL-----RTHMNSSITAFKVGFWRSESA-----ALOREY 297

DB 298 SEVVIPKMPVDPEAQAPKQPPRSSPNTVKRPTKGRERAGKQKPRGKQOLAKRKT 357

QY 298 LRGKRLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNP 357

DB 358 VKEKKAARTLSAILLAPILTWTPYNIWMLV-STFKDCVPETLW-ELGYWLCYVNSTINP 415

QY 358 FLPLCHRRRFQKAFWKILCVTKW 380

DB 416 MCVALCNKAFRDTF-RLLLLCRW 437

## RESULT 4

JT0531  
muscarinic acetylcholine receptor M5 - rat  
C;Species: Rattus norvegicus (Norway rat)



C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C/Accession: JT0531; A3354; C37121  
R/Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.  
Neuron 1, 403-410, 1988

A>Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor.

A/Reference number: JT0530; MUID:90166521; PMID:3272174

A/Accession: JT0531

A/Molecule type: DNA

A/Residues: 1-531 <BON>

A/Cross-references: UNIPROT:P08911; UNIPARC:UIP00001252BF

R/Jialo, C.F.; Themmen, A.P.N.; Joho, R.; Barberis, C.; Birnbaumer, L.  
J. Biol. Chem. 264, 7328-7337, 1989

A>Title: Molecular cloning and expression of a fifth muscarinic acetylcholine receptor.

A/Reference number: A3354; MUID:89214170; PMID:2540186

A/Accession: A3354

A/Molecule type: DNA

A/Residues: 1-531 <LIA>

A/Cross-references: UNIPARC:UIP00001252BF; GB:M22925; NID:G205311; PIDN:AAA41572.1; PID:  
A/Note: The nucleotide sequence for residues 101-120 and the translation 121-140 are non-

A/Note: the authors translated the codon CAG for residue 19 as Glu, AAC for residue 65 a  
R/Kurtenbach, E.; Curtiss, C.A.M.; Pedder, E.K.; Atken, J.; Hulme, E.C.  
J. Biol. Chem. 265, 13702-13708, 1990

A>Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invov  
A/Reference number: A37121; MUID:90337982; PMID:2380182

A/Accession: C37121

A/Status: preliminary

A/Molecule type: protein

A/Residues: 66-128 <KUR>

A/Cross-references: UNIPARC:UIP00001778C5

C/Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotr  
C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F/29-52/Domain: transmembrane #status predicted <TM1>  
F/66-86/Domain: transmembrane #status predicted <TM2>  
F/104-125/Domain: transmembrane #status predicted <TM3>  
F/146-168/Domain: transmembrane #status predicted <TM4>  
F/191-213/Domain: transmembrane #status predicted <TM5>  
F/443-463/Domain: transmembrane #status predicted <TM6>  
F/478-496/Domain: transmembrane #status predicted <TM7>  
F/7,12/Binding site: carbohydrate (Asn) #status predicted

:Query Match 20.0%; Score 410.5; DB 2; Length 531;  
Best Local Similarity 24.6%; Pred. No. 7.1e-28;  
Matches 122; Conservative 92; Mismatches 140; Indels 141; Gaps 15;

Qy 16 VPIAFLMSSFAFMGVNAVILIAFVVDRLRHRSNYFFNLALISFLVLGLIIPYIPH 75  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
30 ITIAVTAVVSLMTIVGNLVIMISFKVNSQLKTNNVYLLSLACADLIIGIFSMNIYTT 89  
Qy 76 VLP-NNNFGSGICWFMLITDYLCTASVNVILISDYDRYSQSVNAVSYRAOHT---GIM 130  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
90 ILMGRVWLGSLACLWLALDYVASNASVMNLLVISPDYFSITRPITYRAKRTPKKRAGM 149  
Qy 131 KIVAQMVAWVILAFLVNGPMILASDSW-----KNSTNTKDCEPGFVTEWILTITMLLEF 185  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
150 IGLA----WLVSFILWAPAILC---WQYLVGRKTPVPDPDECQIQFLSEPTITFTGTAAP 201  
Qy 186 LLPVISAIVFNVOIYWSLWTR-----RALSRCP-----213  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
202 YIPVSVMTILYCIHYRETERKTDLDLOGSDSVAEAKKREPAAQTILLRSFFSCPRPSLA 261  
Qy 214 ----SHAGFTT--SSSASGHHLRA-----GVACRTSNPGIKESA-----247  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
262 QRERNQASWSSRRSRTSTTKTQTATDLSDADWEKAEOVTCSSYPSEDEAKTTDPVFQ 321  
Qy 248 ---ASHRESHPRKSSILVALRTHMNSSI--TAFKVGSFWRSSEAALR-----290  
Db :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
322 MVYKSEAKESPGKESNQETKETVWNRTRTENSDDYDKPYFLSPAHAHRLKSQCVAYKER 381  
Qy 291 -----QREYAELLRGKILAR 305  
Db ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
382 LVVKADGTQFTNNGCRVKIMPSPVSKDPSTKGPPDNLSHQWTQRKRWLVYKERKAAQ 441

Qy	306	SLAILLSAFACWAPYCLFTIVLSYPRTERPKSVWYSIAFWLOWNSFVNPLYPCLCHR	365
Db	442	TL:SAILLAFITWTPTYNIMVLV-STFDCKVCPVTLMH-LGYWLCYVNSTINPICYALCNR	499
Qy	366	RFQAKFWKILCVTKW	380
Db	500	TFRKTF-KLLLLCRW	513
RESULT 5			
S01114			
muscarinic acetylcholine receptor M2, glandular - pig			
N:Alternate names: muscarinic acetylcholine receptor III			
C:Species: Sus scrofa domestica (domestic pig)			
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004			
C:Accession: S01114			
R:Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.			
FEBS Lett. 235, 257-261, 1989			
A:Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonist			
A:Reference number: S01114; MUID:88296835; PMID:3402600			
A:Accession: S01114			
A:Molecule type: DNA			
A:Residues: 1-590 <AKT>			
A:Cross-references: UNIPROT:P11483; UNIPARC:UPI00001252B7; EMBL:X12712; NID:gl1861; PIDN:C			
C:Superfamily: vertebrate rhodopsin			
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem			
F:68-91/Domain: transmembrane #status predicted <TM1>			
F:105-125/Domain: transmembrane #status predicted <TM2>			
F:143-164/Domain: transmembrane #status predicted <TM3>			
F:185-207/Domain: transmembrane #status predicted <TM4>			
F:231-252/Domain: transmembrane #status predicted <TM5>			
F:493-513/Domain: transmembrane #status predicted <TM6>			
F:528-546/Domain: transmembrane #status predicted <TM7>			
Query Match 20.0%; Score 410.5; DB 2; Length 590;			
Best Local Similarity 24.8%; Pred. No. 8e-28;			
Matches 125; Conservative 82; Mismatches 136; Indels 161; Gaps 16;			
Qy	18	LAFLMSSFAFAIMGVNAVIVAVVVDRLNRHSNYFFFLMLAISDFLVGLISIPYIPHLV	77
Db	71	IAFTLGILALVTIIGNILVIVAFKYNKQLKTVNNYFLLSLACADLIIGVISMNLFTYII	130
Qy	78	FN-WNFGSGICFMFLITDYLTCTASVYNIVLISYDRYQSVNAVSYRAQHT----	GIMKI 132
Db	131	MNRWALGNLACDLWLSIDYVNASVWMLLVISFDRIYFSITRPLTYRAKRTTKRAGVMIG	190
Qy	133	VAQWVAVWILAFVNGPMLASDSWKNSTNTKDCPG-----FVTEWYILITIMLEFLL	187
Db	191	LA-----WVISFILWAPAIL---FMQYFVGKRTVPVPGECFIQFLSEPTITFGTAIAAFYM	242
Qy	188	PVISVAYENVVYNSLWKRRALSRCPSHAGF--STTSSASGHLHRAGVACRTSNPGLKE	245
Db	243	PVTIMTI-----LYRWIYKETE-KRTKELAGLQASGTEAEENFVHPETGTSRSCSYELQQ	297
Qy	246	SAASR-----HSES-----	254
Db	298	QSLKRSARKYGRCHFETTKSWKPSAQMDDHSSDSMNNDAAASLENSASSDEEDI	357
Qy	255	---PRRKSSILVSLRTHWN-----SSITAFKV----	278
Db	358	GSETRAIYSIVLKLPGHSITILNSTKLPSDDNLQVPHEELGTVDLERKASKLQAKSMDDG	417
Qy	279	GSFWR-----ESAA-----	LRQ 291
Db	418	GSFQKSFSLPIQESAVDTAKASDVNSVGKTTATLPLSFKEATLAKRFALKTRSOITK	477
Qy	292	REYAEILGRKLARSAILLSAFACWAPYCLFTIVLSYPRTERPKSVWYSIAFWLOWNSFVNPLYPCLCHR	351
Db	478	KRWSLIKEKAAQTLSAILLAFITWTPTYNIMVLV-NTFCDSCIPKTYW-NLGYWLCYI	535
Qy	352	NSFVNPFLYPICHRRFQKAFWKIL	375
Db	536	NSTVNPVYALCNKTFRTFMKLL	559

## RESULT 6

151837 muscarinic receptor - rat  
C/Species: Rattus sp. (rat)  
C/Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Nov-1999  
C/Accession: I51837  
R/Lai, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske  
Adv. Exp. Med. Biol. 287, 313-330, 1991  
A/Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy  
A/Reference number: I51837; MUID:92101806; PMID:1759615  
A/Accession: I51837  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-460 <RES>  
A/Cross-references: UNIPARC:UPI0000046CE7; GB:S73971; NID:g241253; PIDN:AAB20705.1; PID:  
C/Genetics:  
A/Gene: m1  
C/Superfamily: vertebrate rhodopsin

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Query Match      20.0%; Score 410; DB 2; Length 460;
Best Local Similarity 27.4%; Pred. No. 6.7e-28;
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;

QY  5 NSTGILPPAAQVPLAFL--MSSGFAPAIMVGNVAVILAFVVDNRNLHRSNVFFLNLAISD 61
Db  12 NITVLPAGKGPQWVAFIGITIGLLSLATVGNLLVLISFKVNTLKVNNYFLLSLACAD 71

QY  62 FLVGLISIPLYIPHLVLF-NNFGSGICMFWLITDYLCTASVYNNVILISYDRYQSVNAV 120
Db  72 LIIGTFSMNLTYTYLLMGHWALGTLACDLMLALDYVASNASVMNLLISDFRYSVTRPL 131

QY  121 SYRAQHTGINKIVAQWAV-WILAFVNGPMLASDSWKNSTWK-----DCEPGFVTEW 174
Db  132 SYRAKRT--PRRAALMTGLAWLVSFVLWAPAIL---FWQYLVGERTVLAGQCQYIQLSQP 186

QY  175 YLITITMLLEFLPLVTSVAVFNQIYWSLWKR-----RAL-----SRCPSHAGFSTSSS 224
Db  187 IITFGTMAAFYLPVTVMC-----TLWRIYRETNARALAAQGSPTPKGGSSSSSE 242

QY  225 AS-----GHLHRAGVACRT-----RTHMNSSITAFKVGSWFSESA-----ALRQREY 294
Db  243 RSQPGAEGSPESPGRCCR---CCRAPRLLIQAYSWKKEEEDSGMESLTSSEGEEP--G 297

QY  259 SSILVSL-----RTHMNSSITAFKVGSWFSESA-----ALRQREY 294
Db  298 SEVVIRKMPVDSQAQPTKQPPKSSPNTVRPTKKG---RDRGGKGQKPKGKQLAKRKT 354

QY  295 AEILGRKGLARSILAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSF 354
Db  355 FSLVKEKAARTISAILLAFILTWTPNIMVLV-STFKDCVPETLW-ELGYWMLCYNST 412

QY  355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
Db  413 VNPWCYALCNKAPRDTF-RLLLLCRW 437
```

## RESULT 7

A29514 muscarinic acetylcholine receptor M1 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C/Accession: A94518; A94293; A37121; A29514  
R/Bonner, T.I.  
submitted to GenBank, July 1987  
A/Reference number: A94518  
A/Accession: A94518  
A/Molecule type: mRNA  
A/Residues: 1-460 <B01>  
A/Cross-references: UNIPROT:P08482; UNIPARC:UPI00000046CE7  
R/Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.  
Science 237, 527-532, 1987

A/Title: Identification of a family of muscarinic acetylcholine receptor genes.  
A/Reference number: A94293; MUID:87263421; PMID:3037705  
A/Accession: A94293  
A/Molecule type: mRNA  
A/Residues: 1-227;338-460 <B02>  
A/Cross-references: UNIPARC:UPI00001778CE; UNIPARC:UPI00001778CF  
A/Experimental source: cerebral cortex  
A/Note: only a part of the protein translation is given; none of the nucleotide sequen  
R/Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C  
J. Biol. Chem. 265, 13702-13708, 1990  
A/Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues in  
A/Reference number: A37121; MUID:90337982; PMID:2380182  
A/Accession: A37121  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 62-124 <KUR>  
A/Cross-references: UNIPARC:UPI00001778D0  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosph  
F/25-50/Domain: transmembrane #status predicted <TM1>  
F/62-93/Domain: transmembrane #status predicted <TM2>  
F/100-121/Domain: transmembrane #status predicted <TM3>  
F/142-168/Domain: transmembrane #status predicted <TM4>  
F/187-209/Domain: transmembrane #status predicted <TM5>  
F/367-387/Domain: transmembrane #status predicted <TM6>  
F/402-420/Domain: transmembrane #status predicted <TM7>  
F/2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match      20.0%; Score 410; DB 2; Length 460;
Best Local Similarity 27.4%; Pred. No. 6.7e-28;
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;

QY  5 NSTGILPPAAQVPLAFL--MSSGFAPAIMVGNVAVILAFVVDNRNLHRSNVFFLNLAISD 61
Db  12 NITVLPAGKGPQWVAFIGITIGLLSLATVGNLLVLISFKVNTLKVNNYFLLSLACAD 71

QY  62 FLVGLISIPLYIPHLVLF-NNFGSGICMFWLITDYLCTASVYNNVILISYDRYQSVNAV 120
Db  72 LIIGTFSMNLTYTYLLMGHWALGTLACDLMLALDYVASNASVMNLLISDFRYSVTRPL 131

QY  121 SYRAQHTGINKIVAQWAV-WILAFVNGPMLASDSWKNSTWK-----DCEPGFVTEW 174
Db  132 SYRAKRT--PRRAALMTGLAWLVSFVLWAPAIL---FWQYLVGERTVLAGQCQYIQLSQP 186

QY  175 YLITITMLLEFLPLVTSVAVFNQIYWSLWKR-----RAL-----SRCPSHAGFSTSSS 224
Db  187 IITFGTMAAFYLPVTVMC-----TLWRIYRETNARALAAQGSPTPKGGSSSSSE 242

QY  225 AS-----GHLHRAGVACRT-----RTHMNSSITAFKVGSWFSESA-----ALRQREY 294
Db  243 RSQPGAEGSPESPGRCCR---CCRAPRLLIQAYSWKKEEEDSGMESLTSSEGEEP--G 297

QY  259 SSILVSL-----RTHMNSSITAFKVGSWFSESA-----ALRQREY 294
Db  298 SEVVIRKMPVDSQAQPTKQPPKSSPNTVRPTKKG---RDRGGKGQKPKGKQLAKRKT 354

QY  295 AEILGRKGLARSILAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSF 354
Db  355 FSLVKEKAARTISAILLAFILTWTPNIMVLV-STFKDCVPETLW-ELGYWMLCYNST 412

QY  355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
Db  413 VNPWCYALCNKAPRDTF-RLLLLCRW 437
```

## RESULT 8

S47572 muscarinic acetylcholine receptor m3 - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S47572  
R/Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.  
Biochim. Biophys. Acta 1223, 151-154, 1994

A>Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 r

A;Reference number: S47572; MUID:94339178; PMID:8061048

A;Accession: S47572

A>Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-590 <LE>

A;Cross-references: UNIPROT:P41984; UNIPARC:UPI00001252B3; EMBL:U08286; NID:g520465; PID:

C;Superfamily: vertebrate rhodopsin

C;Keywords: neurotransmitter receptor

Query Match 20.0%; Score 409.5; DB 2; Length 590;  
Best Local Similarity 25.0%; Pred.No. 9.8e-28;  
Matches 126; Conservative 83; Mismatches 134; Indels 161; Gaps 17;

Qy 18 LAFIMSFAPAIMVGNAAVLAVFVDNRNLRHRSNYFFNLAIISDFLVGLHSIPIYHPVL 77  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 78 FN-WNGSGGICMFWLITDYLLCTASVYNVLISYDRYQSVSNAVSRAQHT-----GIMKI 132  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 131 MNRWALGNLACDLWLSIDYYASNASVMNLIVISPDYSITSIRPLTYRKRKTKTRAGVMIG 190  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 133 VAQWVAWIIAFLVNGPMILASDWSKNSTWKDCPG-----FWTEWYLITITMLLEFL 187  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 191 LA-----WVISFILWAPAII---FMQYFGKRTVPGECFIQFLSPTTFGTATIAAFYM 242  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 188 PVISVAYFNQIYWSLMKRRALSRCPSHAGF--STTSSSASGHLHRAGVACRTSNPGLKE 245  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 243 PVTIIMI---LYRWIKETE-KRKELAGLQASGTEAEAFNVHPVTGSSRSCSYELQQ 297  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 246 SAASR-----HSSS-----254  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 298 QSMKRARRKYGRCHFETTKSWKPQAEOHQDSDDSNWNNDAAAASSENSASSDEEDI 357  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 255 ---PRKSSLVSRTH---MNS---SITAFKV-----278  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 358 GSTRAIYSIVLKLPGHSTILNSTKLPSSDNLOVPEELGSVGLERKKPKLTQQSQMDGD 417  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 279 GSFWRS-----EGAA-----LRQ 291  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 418 GSQKFSSKLPIQLSESAVDATAKDVSNSVGKTTAILPLSPKEATLAKRPALKTRSQTIK 477  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 292 REYAELLRGRLARSIALILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWF 351  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 478 RKRMSLIKEKAQTLISAILLFIITWTYPYINMLV-NTFCDSCIPKTYW-NLGYWLCYI 535  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 352 NSFVNPLYPLCHRRRFQKAFWKIL 375  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
Qy 536 NSTNPVCVALCNKTFRNTFKMILL 559  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

RESULT 9

A29476

muscarinic acetylcholine receptor M4 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

C;Accession: A29476

R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.  
Biochem. Biophys. Res. Commun. 149, 125-132, 1987.

A;Title: A novel subtype of muscarinic receptor identified by homology screening.

A;Reference number: A29476; MUID:88077068; PMID:3120722

A;Accession: A29476

A:Molecule type: mRNA

A;Residues: 1-589 <BR>

A;Cross-references: UNIPROT:P08483; UNIPARC:UPI0000170853; GB:M18088; NID:g202657; PID:

A;Experimental source: brain

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane F;67-90/Domain: transmembrane #status predicted <TM1>  
F;104-124/Domain: transmembrane #status predicted <TM2>  
F;142-163/Domain: transmembrane #status predicted <TM3>  
F;184-206/Domain: transmembrane #status predicted <TM4>  
F;230-251/Domain: transmembrane #status predicted <TM5>

F;492-512/Domain: transmembrane #status predicted <TM6>  
F;527-545/Domain: transmembrane #status predicted <TM7>

Query Match            19.7%; Score 403; DB 2; Length 589;  
Best Local Similarity   23.8%; Pred. No. 3.e-27;  
Matches 125; Conservative 84; Mismatches 145; Indels 172; Gaps 15;

Qy	4	SNSTGILPPRAAQ-----VPLAFLMSSFAFAIMGVNAVLIAFVDNRNLRHSRYFFLNLA	58
Db	51	NNDSDDPLGGHTIIQQVVVFIAFLTGLFALVTIIGNILVIAFKVNKQLKTAVNYFFLSLA	110
Qy	59	ISDFLVGLGISLPIPHVLPFN-WNFSGICGMFWLLITDYLCTASVYNNIVLISDYRYSQS	117
Db	111	CADLIIGVISWNLTFTTIIMRWALGNACDLWLSIDYVASNVNWLIVISDFRFESYT	170
Qy	118	NAVSYRAOHT----GIMKIYAQMVAWVILAFLVNGPMILASDSWKNSNTTKDCEPG---	169
Db	171	RPLYRAKRTRTKRAGVMIGLA-----WVISFLWAPAIL---FWQYFVGKRTVPPEGCFI	222
Qy	170	-FVTEWTILITMLLEFP LLPVISAAYFNQIYWSLWKRRLSRCPSHAGF--STTSASS	226
Db	223	QFLSEPTITGTATAAFMPYTIMTI-----LYMRIYKETE-KRTKELAGLASGTAEAE	277
Qy	227	GHLRHAGVACTSNPGLKESAASHSESPRKK-----	258
Db	278	NFVHTPGSSSCSSEYLOQGVKR-----SSRKYGRCHEFWFTSKWPSPAEOQMDODHSSSD	334
Qy	259	-----SSILVS LRLTHMNSSI-----	273
Db	335	SWNNDAASAILENASDEEDIGSETRAIYSIVLKLPGHSHILNSTKLPSNDNLQVSNED	394
Qy	274	-----TA FK VGS FWRSSAA-----	288
Db	395	LGTVDVERN AH K LQA QSMGDGCNQDKFT KL P I OLES AVDTGK TSDTNSSADKTTATIP	454
Qy	289	-----LRQEYAEELRGKRLARS LA IL LS A FA IC W AP C LF IV L S	329
Db	455	LSPKEATLAKRFALKTRTSQITRKRMSLIKSKAQTLSAILLAFIITWPNYMVLV-N	513
Qy	330	TYPRTERP KS VWYS IA FWLF N SF NF PL YPLCHRR RFQK AF WK IL	375
Db	514	TFRDSCIPTKYW-NLGWYLCVINSTVNPVCVALCNKTRFTTKMLL	558

RESULT 10  
S10128  
muscarinic acetylcholine receptor M4 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S10128  
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression patterns of five members of the type II muscarinic acetylcholine receptor gene family  
A;Reference number: S04326; MUID:88166632; PMID:3443095  
A;Accession: S10128  
A;Molecule type: DNA  
A;Residues: 1-590 <PCR>  
A;Cross-references: UNIPROT:P20309; UNIPARC:UIPO000050453; EMBL:X15266; NID:g32323; PIDN:  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein  
F;68-95/Domain: transmembrane #status predicted <TM1>  
F;105-131/Domain: transmembrane #status predicted <TM2>  
F;143-164/Domain: transmembrane #status predicted <TM3>  
F;185-207/Domain: transmembrane #status predicted <TM4>  
F;231-252/Domain: transmembrane #status predicted <TM5>  
F;493-513/Domain: transmembrane #status predicted <TM6>  
F;525-546/Domain: transmembrane #status predicted <TM7>  
F;5,6,15,41/Binding site: carbohydrate (asn) #status predicted

Query Match            19.7%; Score 402.5; DB 2; Length 590;  
Best Local Similarity   24.0%; Pred. No. 4.e-27;  
Matches 121; Conservative 86; Mismatches 135; Indels 163; Gaps 16;

Query Match 19.7%; Score 402.5; DB 2; Length 590;  
Best Local Similarity 24.0%; Pred. No. 4e-27;  
Matches 121; Conservative 86; Mismatches 135; Indels 163

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QY 18 LAFLMSSFAFAMVGNVAVILAFVVDNRNLHRSNYFFLNLAISDFLVGLISIPLYPHVL 77
Db 71 IAFITGILAVTIIGNILVIVSFKNVQLKTVNNYFLLSACADLIIGVISMNLFTFYII 130
QY 78 FN-WNFGSGICMFWLITDYLLCTASVNVNVLISVDRIYQSVNASVYRAQHT----GIMKI 132
Db 131 MNRWALGNLACDLWLADLDYVASNASVNNLLVISPDRYFSITRPLTYRAKRTTKRAGVMIG 190
QY 133 VAQVAVVILAFVNGPMILASDSWKNSTNTKDCPEG-----FVTEWVILTIWMLLEFLL 187
Db 191 LA-----WVIFVLWAPAIL---FWQYFVGKRTVPPGECFIQFLUSEPTITFGTAIAAFYM 242
QY 188 PVISVAFNVQIYMSLWK-----LYWRIYKETEKTRELQAGSQTEATEENFVHPTGSSRSCSYELQQQ 205
Db 243 PVIMTI----LYWRIYKETEKTRELQAGSQTEATEENFVHPTGSSRSCSYELQQQ 298
QY 206 -----RRALSRCPSHAGFTT-----SSASGHLHRAQVACRTSNPGLUKES 246
Db 299 SMKRSNRKYGRC--HFWFTTKSWKPSQEQMDQDHSSSDSWNNNDAAAASLENSASSDEED 356
QY 247 AASR-----HS----- 252
Db 357 IGSETRAIYIVLKPCHSTILNSTKLPSDNLQVPEELGMVDLERKADKLOAQKSVDD 416
QY 253 --ESPRRKSGILVSLR-----THMNSSI-----TAFKVGSS-----FWRSESAALR 290
Db 417 GGFPPKFSKLPQLQESAVDTAKTSDVNSVGKSTATLPLSFKEATLAKRFALKTRSQIT 476
QY 291 OREYAEALLRGRKLARSIAILLSPAICWAPYCLPTIVLSTVPTERPCKSVWYSIAFWLQW 350
Db 477 KKRMSLVKEKKAQAQTLAISALLAFIITWTPYINMLV-NTFCDSCIPKTFW-NLGYWLVCY 534
QY 351 FNSVNPFPYPLCHRRFQKAFWKIL 375
Db 535 INSTVNPVCYALCNKTRTFTFKMLL 559

RESULT 11
B29514
muscarinic acetylcholine receptor M3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: B94518; B94293; B37121; B29514
R;Bonner, T.I.
submitted to GenBank, July 1987
A;Reference number: A94518
A;Accession: B94518
A;Molecule type: mRNA
A;Residues: 1-589 <B01>
A;Cross-references: UNIPROT:P08483; UNIPARC:UPI0000163B75
R;Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
A;Reference number: A94293; MUID:87263421; PMID:3037705
A;Accession: B94293
A;Molecule type: mRNA
A;Residues: 1-269;463-589 <B02>
A;Cross-references: UNIPARC:UPI00001778C1; UNIPARC:UPI00001778C2
A;Experimental source: cerebral cortex
A;Note: only a part of the protein translation is given; none of the nucleotide sequence
R;Kurténbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invc
A;Reference number: A37121; MUID:90337982; PMID:2380182
A;Accession: B37121
A;Status: preliminary
A;Molecule type: protein
A;Residues: 104-166 <KUR>
A;Cross-references: UNIPARC:UPI00001778C3
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F;67-90/Domain: transmembrane #status predicted <TM1>
F;104-124/Domain: transmembrane #status predicted <TM2>
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F;142-163/Domain: transmembrane #status predicted <TM3>
F;184-206/Domain: transmembrane #status predicted <TM4>
F;230-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;6;15;41;48;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.6%; Score 402; DB 2; Length 589;
Best Local Similarity 23.8%; Pred. No. 4.4e-27;
Matches 125; Conservative 84; Mismatches 145; Indels 172; Gaps 15;

QY 4 SNTGILPPAAQ-----VPLAFMSSFAFAMVGNVAVILAFVVDNRNLHRSNYFFLNLA 58
Db 51 SNTDSSDPLGGHTIWQVVFIAFLTGLFALVTIIGNILVIVAFKNVQLKTVNNYFLLSLA 110
QY 59 ISDFLVGLISIPLYPHVLEN-WNFGSGICMFWLITDYLLCTASVNVNVLISVDRIYQSVS 117
Db 111 CADLIIGVISMNLFTFYIIMNRWALGNLACDLWLSIDYVASNASVNNLLVISPDRYFSIT 170
QY 118 NAVSYRAQHT----GIMKIQAQVAVVILAFVNGPMILASDSWKNSTNTKDCPEG---- 169
Db 171 RPLTYRAKRTTKRGMVIGLA-----WVIFVLWAPAIL---FWQYFVGKRTVPPGECFI 222
QY 170 -FVTEWVILTIWMLLEFLLPVISVAVPNVQIYVLSLWKRALSRCPSHAGF--STSSAS 226
Db 223 QFLSEPTITFGTAIAAFYMPDVIMTI----LYWRIYKETE-KRTKELAGLQASGTEAEAE 277
QY 227 GHLHRAQVACRTSNPGIKESASRHSSEPRK-----SSILVSLRTHMNSSI----- 258
Db 278 NFVHPTGSSRSCSYELQQGVKR---SSRKYGRCHFVFTTKSWKPSAQMDQDHSSSD 334
QY 259 -----SWNNDDAAAASLENSASSDEEDIGSETRAIYIVLKPCHSTILNSTKLPSDNLQVSNED 394
Db 274 -----TAFKVGSSFWSESA----- 288
QY 395 LGTVVDVERNAHKLQAKSMGDGNCQDKFTKLPQLQESAVDTGKTSNTSSADKTTATLP 454
Db 289 -----LRQREYAEALLRGRKLARSIAILLSPAICWAPYCLPTIVLS 329
QY 455 LSPKEATLAKRFALKTRSQITKKRMSLVKEKKAQAQTLAISALLAFIITWTPYINMLV-N 513
QY 330 TYPTERTPKSVWYSIAFWLQWFMNSFVNPFLYPLCHRRFQKAFWKIL 375
Db 514 TPCDSCIPKTYW-NLGYWLVCYINSTVNPVCYALCNKTRTFTFKILL 558

RESULT 12
A55019
muscarinic acetylcholine receptor, M3 isoform - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: A55019
R;Gadbut, A.P.; Galper, J.B.
J. Biol. Chem. 269, 25823-25829, 1994
A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium ar
A;Reference number: A55019; MUID:95014393; PMID:7929287
A;Accession: A55019
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-639 <GAD>
A;Cross-references: UNIPROT:P49578; UNIPARC:UPI00001252B4; GB:L10617; NID:9530097; PID
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

Query Match 19.6%; Score 401; DB 2; Length 639;
Best Local Similarity 24.4%; Pred. No. 5.9e-27;
Matches 124; Conservative 84; Mismatches 136; Indels 164; Gaps 16;

QY 16 VPLAFMSSFAFAMVGNVAVILAFVVDNRNLHRSNYFFLNLAISDFLVGLISIPLYPH 75
Db 117 VLI AFLTGIITVLTIIIGNILVIVSFKNVQLKTVNNYFLLSACADLIIGVISMNLFTTY 176
```



Job time : 26 secs

```
QY 214 ----SHAGFTT---SSASGHLHRAG-----VACRT-----SNPGLK 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 263 QRENNQASWSSRRSISITGKPSQATGPSANWAKAEQLTTCSSYPSSDEDEKPADPVLQ 322
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 ESASRHSBPRKRSILVSLRTHMSSI--TAFKVGSWRSESALR-----290
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 323 VVYKSGKSPGSEFSAEETEETFVKAETESDYDTPNYLLSPAAAHRPKSKQCVAYKFR 382
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 -----OREYAEALLRGRKLAR 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 383 LVVKADGNQETNNGCHKVKIMPCFPFVAKPEPTKGLNPNPDSHOMTKRKRVVLVKKAKAQ 442
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 306 SLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPELYPLCHR 365
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 443 TLSAILLAFIITWTPYNNIMLV-STPCDKCVPVTLWH-LGYWLCYVNSTVNPICYALCNR 500
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 366 FOKAFKWLICVTWK 380
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 501 TFRKTF-KMILLCRW 514

RESULT 15
S71323
alpha-1A adrenergic receptor - Japanese medaka
C;Species: Oryzias latipes (Japanese medaka)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C;Accession: S71323
R;Tasuoka, A.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 235, 501-507, 1996
A;Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Me
A;Reference number: S71323; PMID:96184522; PMID:8654394
A;Accession: S71323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <YAS>
A;Cross-references: UNIPARC:UPI00001778AD; EMBL:D63859
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
C;Superfamily: vertebrate rhodopsin

Query Match 19.2%; Score 392.5; DB 2; Length 477;
Best Local Similarity 28.0%; Pred. No. 2.3e-26;
Matches 115; Conservative 65; Mismatches 145; Indels 85; Gaps 15;

QY 4 SNSTGILPP---AAQVPLAFLMSSPAFAIMVGNNAVILAFVVDNRNLRHSNYFFNLNLA 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 SNGSHVLAPENVTKAVVLGVLGIFILFGVIGNILVLSVCHRLQTVTYFIVNLAV 77
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 SDFVLGLISIP-L-YIPHVLFNWNPFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVN 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 ADLLLSLTVLPFSAIFELDRWVGRVFCNIWAAVDVLCCTASTMSLCVISVDRIYIGVSY 137
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 AVSYRAQHTGIMKIVAOQWAVVILAFVN-GPMILASDSWKNSTNTKD--C---EPGFV 171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 PLRYPAIMTKRRALLAVML-LWLSLVIIISIGPLF----GWKEPADETVCKITEEPGYA 192
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 TEWYLITMLLEFLPLVISVAVFNVOIYNSLMKRRALSRCPSHAGPSTTSSASGHLHR 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 -----IFSAGSFYLPAILAMYCRVY-----215
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 AGVACRTSNFLKESASRHSBPRKRSILVSLRTHMSSIITAFKVGSWRSESALRQ 291
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 --VVAQKESRGLKSGQIKESDSQ-----VILRMHNGNTV-----SEDEALRS 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 REYAE-----LRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAF 346
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 RTHFALRLKFRSREKKAATLGIIVGCVLCWLPFFLVPFIGSIFP-AYRPSDTVFKITF 317
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 WLOWNFNSVNPFLPLCHRRFQKAFWKIL---CVTKWPA-----LSQNQS 388
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 318 WLGYFNSCINPIIYLCNQEFKAFQSLGLGVHCLRWTPRAHHHLSVGQS 367
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: May 24, 2006, 13:35:04
```

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2006, 13:31:50 ; Search time 147 Seconds  
(without alignments)  
2460.416 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPAALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result #	No.	Score	Query Match	Length	DB	ID	Description
1	2035	85.2	391	2	Q91ZY2	MUSCULU	Q91ZY2 mus musculus
2	1745	85.2	391	2	Q91ZY1	RAT	Q91ZY1 rattus norv
3	1372.5	67.0	390	2	Q96LD9	HUMAN	Q96LD9 homo sapien
4	1372	67.0	262	2	Q2M2N7	MUSCULU	Q2M2N7 mus musculus
5	1370.5	66.9	390	1	HRH4	HUMAN	Q9H3N8 homo sapien
6	1370.5	66.9	390	2	Q4G0I6	HUMAN	Q4G0I6 homo sapien
7	1357.5	66.3	390	2	Q3V8G8	MACACA	Q3V8G8 macaca fasc
8	1311.5	64.0	390	2	Q3WNV9	FIG	Q3WNV9 sus scrofa
9	1238	60.4	389	2	Q91ZY3	CAVPO	Q91ZY3 cavia porce
10	733.5	35.8	414	2	Q4RKY3	TETNG	Q4RKY3 tetraodon n
11	722.5	35.3	445	1	HRH3	HUMAN	Q9Y5N1 homo sapien
12	722.5	35.3	445	1	HRH3	HUMAN	Q348M6 homo sapien
13	721	35.2	445	1	HRH3	CAVPO	Q91ZY3 cavia porce
14	718.5	35.1	445	2	Q865B1	MACMU	Q865B1 macaca mula
15	716.5	35.0	445	1	HRH3	RAT	Q9GYN8 rattus norv
16	715.5	34.9	445	1	HRH3	MUSCULU	P8H406 mus musculus
17	715.5	34.9	445	2	Q540F3	MUSCULU	Q540F3 mus musculus
18	713.5	34.8	445	2	Q9G535	PHOSU	Q9G535 phodopus su
19	712.5	34.8	341	2	Q4RVG9	TETNG	Q4RVG9 tetraodon n
20	709.5	34.6	413	2	Q541U0	RAT	Q541U0 rattus norv
21	704.5	34.4	473	2	Q2MZJ3	BRARE	Q2MZJ3 brachydanio
22	700.5	34.2	406	2	Q3USH0	MUSCULU	Q3USH0 mus musculus
23	691.5	33.8	406	2	Q5G534	PHOSU	Q5G534 phodopus su
24	665.5	32.5	365	2	Q9WY01	HUMAN	Q9WY01 homo sapien
25	665.5	32.5	373	2	Q9WXZ9	HUMAN	Q9WXZ9 homo sapien
26	591	28.9	497	2	Q2VJ18	RAT	Q2VJ18 rattus norv
27	584	28.5	465	2	Q2VJ17	RAT	Q2VJ17 rattus norv
28	569	27.8	344	2	Q5PPG3	RAT	Q5PPG3 rattus norv
29	547	26.7	174	2	Q6J9J4	9PRIM	Q6J9J4 gorilla gor
30	543	26.5	175	2	Q6J9J5	PANTR	Q6J9J5 pan troglod
31	492.5	24.0	301	2	Q8WY00	HUMAN	Q8WY00 homo sapien

32	492.5	24.0	309	2	Q8NI49	HUMAN	Q8NI49 homo sapien
33	443	21.6	443	2	Q4SAC4	TETNG	Q4SAC4 tetraodon n
34	418	20.4	460	1	ACM1	MACMU	P56489 macaca mula
35	417.5	20.4	584	2	Q61W39	CAEBR	Q61W39 caenorhabdi
36	416	20.3	481	2	Q5U3D9	BRARE	Q5U3D9 brachydanio
37	415.5	20.3	530	2	Q8VH24	CAVPO	Q8VH24 cavia porce
38	414.5	20.2	532	1	ACM5	MACMU	P56490 macaca mula
39	413	20.2	454	2	Q96RH1	HUMAN	Q96RH1 homo sapien
40	413	20.2	460	1	ACM1	HUMAN	P11229 homo sapien
41	413	20.2	460	1	ACM1	PIG	P04761 sus scrofa
42	413	20.2	460	2	Q53XZ3	HUMAN	Q53XZ3 homo sapien
43	413	20.2	460	2	Q5R949	PONPY	Q5R949 pongo pygma
44	410.5	20.0	502	2	Q4PLW4	LEPMA	Q4PLW4 lepomis mac
45	410.5	20.0	531	1	ACM5	RAT	P08911 rattus norv

ALIGNMENTS

RESULT 1  
Q91ZY2 MOUSE  
ID Q91ZY2 MOUSE PRELIMINARY; PRT; 391 AA.  
AC Q91ZY2;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DE 21-FEB-2006, entry version 23.  
DE Histamine H4 receptor.  
GN Name=Hrh4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC SFRAIN-BALB/c;  
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC EMBL; AF358859; AAK97380.1; -; mRNA.  
DR Ensembl; ENSMUSG0000037346; Mus musculus.  
DR MGI; MGI:2429635; Hrh4.  
DR GO; GO:0005615; C:extracellular space; RCA.  
DR GO; GO:0005887; C:integral to plasma membrane; IC.  
DR GO; GO:0005624; C:membrane fraction; IDA.  
DR GO; GO:0004969; F:histamine receptor activity; IDA.  
DR GO; GO:0001594; F:rhodopsin-like receptor activity; RCA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; RCA.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR InterPro; IPR002076; GPCR\_Rhodpsn.  
DR InterPro; IPR008102; Histam\_H4\_rcpt.  
DR PANTHER; PTHR19266:SF82; Histamrecept\_H4; 1.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHHODOPSN.  
DR PRINTS; PR01726; HISTAMINEH4R.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Membrane; Receptor; Transducer;  
KW Transmembrane.  
SQ SEQUENCE 391 AA; 44249 MW; 59EC73CB5214C5E0 CRC64;

Query Match 99.4%; Score 2035; DB 2; Length 391;

Best Local Similarity 99.7%; Pred. No. 2e-138;

Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPAALSONQSVSS 60

Db 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPAALSONQSVSS 60

```

QY 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLIITDYLLCTASVNVIVLISYDRYQSVNAV 120
Db 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLIITDYLLCTASVNVIVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIIVAOQVAVWVILAFVNGPMLASDSWKNSNTKDCPEPGFVTEWYILITIT 180
Db 121 SYRAQHTGIMKIIVAOQVAVWVILAFVNGPMLASDSWKNSNTKDCPEPGFVTEWYILITIT 180
QY 181 MLLEFLLPVSIVAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
Db 181 MLLEFLLPVSIVAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
QY 241 PGKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGFWFSESAAALRQREYAEALLRG 300
Db 241 PGKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGFWFSESAAALRQREYAEALLRG 300
QY 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYISIAFWLQFNFSVNPFLY 360
Db 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYISIAFWLQFNFSVNPFLY 360
QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

RESULT 2
C912YL RAT
ID Q912YL RAT PRELIMINARY; PRT; 391 AA.
AC Q912YL;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 22.
DE Histamine H4 receptor.
GN Name:Hrh4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AF358860; AAK97381.1; -; mRNA.
CC Ensembl; ENSRNOG0000016887; Rattus norvegicus.
CC RGD; 620631; Hrh4.
CC DR GO; 0004969; F:histamine receptor activity; IDA.
CC DR GO; 0006954; P:inflammatory response; IMP.
CC DR GO; 0006276; GPCR_Rhodpsn.
CC DR InterPro; IPR000276; GPCR_Rhodpsn.
CC DR PANTHER; PTHR19266:SF82; Histamine_recept_H4; 1.
CC DR Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR01726; GPCRHHODPSN.
CC DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
CC DR G-protein coupled receptor; Membrane; Receptor; Transducer;
CC Transmembrane.
CC SEQUENCE 391 AA; 44023 MW; C707BA6E39CFED41 CRC64;

Query Match 85.2%; Score 1745; DB 2; Length 391;
Best Local Similarity 84.9%; Pred. No. 1.5e-117;
Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

QY 1 MSENSTGILPPAAQVPLAFILMSSFAFAIMVGNVAVILAFVVDRLNRHRSNYFFLNLAIS 60

```

```

Db 1 MSENSTGILPPAAQVPLAFILMSSFAFAIMVGNVAVILAFVVDRLNRHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLIITDYLLCTASVNVIVLISYDRYQSVNAV 120
Db 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLIITDYLLCTASVNVIVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIIVAOQVAVWVILAFVNGPMLASDSWKNSNTKDCPEPGFVTEWYILITIT 180
Db 121 SYRAQHTGIMKIIVAOQVAVWVILAFVNGPMLASDSWKNSNTKDCPEPGFVTEWYILITIT 180
QY 181 MLLEFLLPVSIVAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
Db 181 MLLEFLLPVSIVAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
QY 241 PGKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGFWFSESAAALRQREYAEALLRG 300
Db 241 PGKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGFWFSESAAALRQREYAEALLRG 300
QY 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYISIAFWLQFNFSVNPFLY 360
Db 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYISIAFWLQFNFSVNPFLY 360
QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

RESULT 3
Q96LD9 HUMAN
ID Q96LD9 HUMAN PRELIMINARY; PRT; 390 AA.
AC Q96LD9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 20.
DE Histamine receptor H4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21106319; PubMed=11179435;
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,
RA Rauser L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RT "Discovery of a novel member of the histamine receptor family.";
RL Mol. Pharmacol. 59:427-433(2001).
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AY008280; AAL09297.1; -; mRNA.
CC Ensembl; ENSG00000134489; Homo sapiens.
CC DR GO; 0016021; C:integral to membrane; IEA.
CC DR GO; 0016020; C:membrane; IEA.
CC DR GO; 0004872; F:receptor activity; IEA.
CC DR GO; 0001584; F:rhodopsin-like receptor activity; IEA.
CC DR GO; 0007186; P:G-protein coupled receptor protein signalin. .; IEA.
CC DR GO; 0007165; P:signal transduction; IEA.
CC DR InterPro; IPR000276; GPCR_Rhodpsn.
CC DR PANTHER; PTHR19266:SF82; Histamine_recept_H4; 1.
CC DR Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR00237; GPCRHHODPSN.
CC DR PRINTS; PR01726; HISTAMINEH4R.
CC DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
CC DR G-protein coupled receptor; Membrane; Receptor; Transducer;
CC Transmembrane.
CC SEQUENCE 390 AA; 44470 MW; CC82B5D30D216C66 CRC64;

```



Query Match 67.0%; Score 1372.5; DB 2; Length 390;  
Best Local Similarity 68.1%; Pred. No. 1.1e-90;  
Matches 267; Conservative 41; Mismatches 81; Indels 3; Gaps 2;

QY 1 MSESNGILPPAAQVPLAFMSGSAFAIMVGNVILAFVDRNLHRNSYFFLNLAIS 60  
DB 1 MDTNSTINLSLSTRTVTLAFMSLVAFIMGLNALVILAFVDRNLHRNSYFFLNLAIS 60

QY 61 DFLVGLISIPYIPIHVLFWNNFGSGICMFWLITDYLCTASVYNIVLISYDRYSQSVNAV 120  
DB 61 DFFVGVISIPYIPIHTLFEWDFGKEICVFWLITDYLCTASVYNIVLISYDRYSVNAV 120

QY 121 SYRAQHTGIMKIYQAVQVAVWILAFVNGPMLASDSWKNSTNTKDCPGFVTEWYILITIT 180  
DB 121 SYRTQHTGVILKIVTLVAVVWLVAFVNGPMLVSESWKDEGS--ECBPGFSEWYILAIT 178

QY 181 MLLEFLLPVSIVAYENVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSN 240  
DB 179 SFLEFVPIVLVAYFNNIYWSLWKRDHLRCQSHPGLTAVSNIICHSFGRLSRRSL 238

QY 241 PGLKESAASHSESPPRRKSSILVSLRTHMNSSITAFKVGFSWRSESAALRQREYAEILLRG 300  
DB 239 SASTVPASHSESRRQKSSLSMFSRTKMSNTIASKGFSQSDSVALHQREHVELLRA 298

QY 301 RKLARSLAILLSAPALCWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWFSFNVPFLY 360  
DB 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWFSFNVPFLY 358

QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
DB 359 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 390

## RESULT 4

Q2M2N7\_MOUSE PRELIMINARY; PRT; 262 AA.  
AC Q2M2N7;  
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.  
DT 21-FEB-2006, sequence version 1.  
DT 21-FEB-2006, entry version 1.  
DE Hrh4 protein.  
GN Names=Hrh4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=PCR rescued clones; DOI=10.1073/pnas.242603899;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]

RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=PCR rescued clones;  
RG NIH MGC Project;  
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.  
CC  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
DR EMBL; BC111862; AAI11863.1; -, mRNA.  
SQ SEQUENCE 262 AA; 29860 MW; 1A0CAF2085E09779 CRC64;

Query Match 67.0%; Score 1372; DB 2; Length 262;  
Best Local Similarity 99.6%; Pred. No. 7.7e-91;  
Matches 261; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 130 MKTIAQVAVWILAFVNGPMLASDSWKNSTNTKDCPGFVTEWYILITITMLLEFLLPV 189  
DB 1 MKTIAQVAVWILAFVNGPMLASDSWKNSTNTKDCPGFVTEWYILITITMLLEFLLPV 60

QY 190 ISVAYFNQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSNPGLKESAAS 249  
DB 61 ISVAYFNQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSNPGLKESAAS 120

QY 250 RHESPPRRKSSILVSLRTHMNSSITAFKVGFSWRSESAALRQREYAEILLRGRKLARSLAI 309  
DB 121 RHESPPRRKSSILVSLRTHMNSSITAFKVGFSWRSESAALRQREYAEILLRGRKLARSLAI 180

QY 310 LLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWFSFNVPFLYPLCHRRFQK 369  
DB 181 LLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWFSFNVPFLYPLCHRRFQK 240

QY 370 AFWKILCVTKWPALSONQSVSS 391  
DB 241 AFWKILCVTKWPALSONQSVSS 262

## RESULT 5

HRH4\_HUMAN STANDARD; PRT; 390 AA.  
ID HRH4\_HUMAN  
AC Q9H3N8; Q9GZQ0;  
DT 01-JUN-2001, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2001, sequence version 2.  
DT 07-MAR-2006, entry version 43.  
DE Histamine H4 receptor (HRH4) (GPRV53) (G-protein coupled receptor 105)  
DE (GPCR105) (SP9144) (AXOR35).  
GN Name=HRH4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RX MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;  
RA Oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.;  
RT "Molecular cloning and characterization of a novel type of histamine  
RT receptor preferentially expressed in leukocytes";  
RT J. Biol. Chem. 275:36781-36786(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.  
RC TISSUE=Leukocyte;  
RX MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;  
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
RT "Molecular cloning and characterization of a new human histamine  
RT receptor, HRH4";  
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RA Jones P.G., Wu S., Betty M.;  
RT "Cloning of a novel histamine receptor";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.



QY 301 RKLARSLAIIISAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360  
 DB 299 RRLAKSLAIIIGVAVCWAPYSLFTIVLSFFSYSSATGPKSVWYIAFWLQWNSFVNPLY 358  
 QY 361 PLCHRRFQKAFWKILCVTKWPKALSO-NQSVSS 391  
 DB 359 PLCHRRFQKAFWKILCVTKWPKALSO-NQSVSS 390

RESULT 6  
 ID Q4G016 HUMAN PRELIMINARY; PRT; 390 AA.  
 AC Q4G016;  
 DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.  
 DT 30-AUG-2005, sequence version 1.  
 DT 21-FEB-2006, entry version 8.  
 DE Histamine H4 receptor.  
 GN Name=HRH4;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones, and Synthetic constructs;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.F., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Synthetic constructs;  
 RG NIH MGC Project;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RG NIH MGC Project;  
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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 CC -----  
 CC EMBL; BC069136; AAH69136.1; -; mRNA.  
 DR EMBL; BC112348; AAH12349.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR008102; Histam\_H4\_rcpt.

DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GCRRHODOPSN.  
 DR PRINTS; PR01726; HISTAMINEH4.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Membrane; Receptor; Transducer;  
 KW Transmembrane.  
 SQ SEQUENCE 390 AA; 44496 MW; C986B8AE7FF912C3 CRC64;

Query Match 66.9%; Score 1370.5; DB 2; Length 390;  
 Best Local Similarity 68.1%; Pred. No. 1.5e-90;  
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMLSSFAFIMVGNVAVILAFVVDRLNLRHSYFFLNLAIS 60  
 DB 1 MPDNTSTINLSLSTRTVLAFFMSLVAFIMLGNALVILAFVVDKLNLRHSYFFLNLAIS 60  
 QY 61 DFLVGLISILYIPIHVLNFFNFGSGICMFWLITDYLCTASVYVNIIVLISYDRYOSVSNV 120  
 DB 61 DFFVGVISIPIYIPHTLFENDFGKEICVFWLITDYLCTASVYVNIIVLISYDRYOSVSNV 120  
 QY 121 SYRAQTGIMKIIVAQVAVVILAFVNGPMILASDSWKNSTNTKDCPFTVEWYILTIT 180  
 DB 121 SYRTQHTGVLKIVTLVAVVLAFLVNGPMLVSESWKDEGS--ECBPGFSEWYILAIT 178  
 QY 181 MLLEFLPLVISVAYFVQIYVSLWKRLALSRCPSHAGFSITSSASGHLHAGVACRTSN 240  
 DB 179 SFLEFVPIVILVAYFNNIYVSLWKRLALSRCPSHAGFSITSSASGHLHAGVACRTSN 238  
 QY 241 PGLKESAAARHSRSPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILRG 300  
 DB 239 SASTEVPAHFSEQRKSSLMFSSRTKMSNTTASKMGSEFSQSDSVALHQREHVELLRA 298  
 QY 301 RKLAISLAIIISAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360  
 DB 299 RRLAKSLAIIIGVAVCWAPYSLFTIVLSFFSYSSATGPKSVWYIAFWLQWNSFVNPLY 358  
 QY 361 PLCHRRFQKAFWKILCVTKWPKALSO-NQSVSS 391  
 DB 359 PLCHRRFQKAFWKILCVTKWPKALSO-NQSVSS 390

RESULT 7  
 Q3V8G8 MACFA  
 ID Q3V8G8 MACFA PRELIMINARY; PRT; 390 AA.  
 AC Q3V8G8;  
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
 DT 11-OCT-2005, sequence version 1.  
 DT 21-FEB-2006, entry version 7.  
 DE Histamine H4 receptor.  
 GN Name=H4;  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopitheidae; Cercopitheciae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=15968139; DOI=10.1254/jphs.SC0050033;  
 RA Oda T., Matsumoto S., Matsumoto M., Takasaki J., Kamohara M., Soga T.,  
 RA Hiyama H., Kobori M., Kato M.;  
 RT "Molecular cloning of monkey histamine H4 receptor."  
 RL J. Pharmacol. Sci. 98:319-322(2005).  
 CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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 CC -----  
 CC EMBL; AB189711; BAB16558.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.

DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . ; IEA.  
DR GO: 0007165; P: signal transduction; IEA.  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR InterPro: IPR008102; Histamm\_H4\_rcpt.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHHODOPSIN.  
DR PRINTS: PR01726; HISTAMINEH4R.  
DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE: PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
DR PROSITE: PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Membrane; Receptor; Transducer;  
KW Transmembrane.  
SQ SEQUENCE 390 AA; 4463 MW; 334F219F33F209AD CRC64;

Query Match 66.3%; Score 1357.5; DB 2; Length 390;  
Best Local Similarity 67.6%; Pred. No. 1.3e-89;  
Matches 265; Conservative 42; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAIMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60  
DB 1 MPDINSTINLSLSTRITLAFMSLLAFALMGNVILAFVVDNLRHRSNYFFLNLAIS 60

QY 61 DFLVGLISIPLYPHLVFNWFGGICMFWLITDYLLCTASVNVILSDRYQSVNAV 120  
DB 61 DFFVGVISIPLYIPHMLFEWDFGKEICVFWLITDYLLCTASVNVILSDRYLSVNAV 120

QY 121 SYRAQHTGIMKIQAQVAVVILAFVNGPMLASDSKNSNTKDCPFGFVTEWYILTIT 180  
DB 121 SYRQHTGILKIVLMAVAVVILAFVNGPMLILVSETWKDEGS--ECPEGFSEWYIVAIT 178

QY 181 MLLEFLLPVISVAVFVQIYWSLWKRRALSRCPHAGFSTTSSASGHLHRAGVACRTSN 240  
DB 179 SFLEFLIPVILVAVFNNIYWSLWKRDHLSRCQSPHGPVAVSSNCQSPRCGLSSRGSL 238

QY 241 PGLKESAAHSRSPRRKSSILVLRTHMSSITAFKVGFWRSSESAALQREYAEILLRG 300  
DB 239 SASTEMVSLHSEQRKSSLMYSLRTKMSNRISAKSGFSQSDSVGLQRHAEALLRA 298

QY 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPF 360  
DB 299 RLAKLSAILLGFAVCWAPYSLFTIVLSYSETGSKSVWYIAFWLQWNSFVNPF 358

QY 361 PLCHRRFQKAFWKILCVTKWPALS-QNQSVSS 391  
DB 359 PLCHKRFQKAFKIFCIKKQPLSPHSRVSS 390

RESULT 8  
Q8WNV9\_PIG  
ID Q8WNV9\_PIG PRELIMINARY; PRT; 390 AA.  
AC Q8WNV9;  
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2002, sequence version 1.  
DT 21-FEB-2006, entry version 19.  
DE Histamine H4 receptor.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue: Spleen;  
RX MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;  
RA Oda T., Matsumoto S., Masuno Y., Takasaki J., Matsumoto M.,  
RA Kamohara M., Saito T., Ohishi T., Soga T., Hiyama H., Matsushima H.,  
RA Furuichi K.;  
RT "cDNA cloning and characterization of porcine histamine H4 receptor.";  
RL Biochim. Biophys. Acta 1575:135-138 (2002).  
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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CC -----  
DR EMBL: AB053300; BAB83078.1; -; mRNA.  
DR GO: 0016021; C: integral to membrane; IEA.  
DR GO: 0016020; C: membrane; IEA.  
DR GO: 0004872; F: receptor activity; IEA.  
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . ; IEA.  
DR GO: 0007165; P: signal transduction; IEA.  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR InterPro: IPR008102; Histamm\_H4\_rcpt.  
DR PANTHER: PTHR19266:SF82; Histamine\_recept\_H4; 1.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHHODOPSIN.  
DR PRINTS: PR01726; HISTAMINEH4R.  
DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE: PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Membrane; Receptor; Transducer;  
KW Transmembrane.  
SQ SEQUENCE 390 AA; 4463 MW; BC8FD363A6F44D3F CRC64;

Query Match 64.0%; Score 1311.5; DB 2; Length 390;  
Best Local Similarity 65.9%; Pred. No. 2.7e-86;  
Matches 259; Conservative 33; Mismatches 96; Indels 5; Gaps 3;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAIMVGNVILAFVVDNRNLRHRSNYFFLNLA 58  
DB 1 MSAINDTNTPLNTRIALAFMLSLALLVILMGNVILAFVVDNLRHRSNYFFLNLA 60

QY 59 ISDFLVGLISIPLYPHLVFNWFGGICMFWLITDYLLCTASVNVILSDRYQSVSN 118  
DB 61 ISDFVGVISIPLYIPHTLFKWKLEDNICAFMLIIDYLLCTASVNVILSDRYQSVSN 120

QY 119 AVSYRAQHTGIMKIQAQVAVVILAFVNGPMLASDSKNSNTKDCPFGFVTEWYILT 178  
DB 121 AVSYRQHTGILKIVLMAVAVVILAFVNGPMLVSEAWKQ--GKQDCEFGFLKEWVLA 178

QY 179 ITMLLEFLLPVISVAVFVQIYWSLWKRRALSRCPHAGFSTTSSASGHLHRAGVACRT 238  
DB 179 ITLFFELAPVLLVAVFNNIYWSLWKRGHLSCQSHGLTPVSSGSGWGHSPRCGLFSRT 238

QY 239 SNPLKESAAHSRSPRRKSSILVLRTHMSSITAFKVGFWRSSESAALQREYAEILL 298  
DB 239 SLSDPKESAAHSRSPRRKSSILVLRTHMSSITAFKVGFWRSSESAALQREYAEILL 297

QY 299 RGRKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPF 358  
DB 298 RARKLARSAILLGFAVCWAPYSLFTIVLSYSETGSKSVWYIAFWLQWNSFVNPF 357

QY 359 LYPCLHRRFQKAFWKILCVTKWPALSQNQSVSS 391  
DB 358 LYPCLCHKRFQKAFKIFCIKKQPLSHNRSTSS 390

RESULT 9  
Q91ZY3\_CAVPO  
ID Q91ZY3\_CAVPO PRELIMINARY; PRT; 389 AA.  
AC Q91ZY3;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 21-FEB-2006, entry version 20.  
DE Histamine H4 receptor.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
OC Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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CC -----
CC EMBL; AF358858; AAK97379.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR008102; Histamin_H4_rcpt.
DR PANTHER; PTHR19266:SF82; Histamine_recept_H4; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
SQ SEQUENCE 389 AA; 44512 MW; 51AF32FD6F1C3E4F CRC64;
Query Match 60.4%; Score 1238; DB 2; Length 389;
Best Local Similarity 62.5%; Pred. No. 5.3e-81;
Matches 245; Conservative 43; Mismatches 100; Indels 4; Gaps 3;
Qy 1 MSESNTGILPPAAQVPLAFILMSFAFAIMVGNVAVILAFVVDRLNRHRSNYFFLNLAIS 60
Db 1 MLANNST-IALTSIKISITFLMSLLATAIMLGNVVILAFVDRNRHRSNYFFLNLAIA 59
Qy 61 DFLVGLISIPLYIPIHVLNPNFGSGICMPFWLITDYLLCTASVYVILSYDRYQSVSNV 120
Db 60 DFFVGAIAIPLIYIPSSLYTMTSGKQACVFWLITDYLLCTASVYVILSYDRYQSVSNV 119
Qy 121 SYRAQGTGIMKIVAOVAVVILAFVNGPMLIASDSKNSNTKDCRPGFVTEWYVILIT 180
Db 120 WYRAQSGTGWKIATQMAVIFSWTNGPMLIISDSQNSTT--ECBPGFLKKWYFALPT 177
Qy 181 MLLEFLPLVISVAYFNVQIYMSLWKRLSRALSCPSHAGF-STSSSSASGHLHRAGVACRTS 239
Db 178 SLLEFLPLILVAVFSAHIYMSLWKREKSLRCLSHPLVPSDSSSDHGHSRCQPDPSRAT 237
Qy 240 NPGKESAASSHSSPRKSKILSVLRTHMNSITAFKVGFWFSESAALRQREYAEALLR 299
Db 238 LPARKETTASIGSDKSRKSLFISIRAYKNSVIAKMGFLSHSDSLAQOREHIELER 297
Qy 300 GRKLARSIALLSAFLCAWAPCYCLFTVILSTYPRTERPKSVVYVIAFWLQFNFSVNPFL 359
Db 298 ARKLAKSLAILLAALFAICWAPYSLTTVIYSPFPBRNLTKSTWYHTAFWLQFNFSVNPFL 357
Qy 360 YPLCHRRFQKAFWKILCVTKWPAISQNSQSVSS 391
Db 358 YPLCHKRFQKAFKILPVRRQSTPPHNRISIT 389
RESULT 10
QARKY3 TETNG
ID QARKY3 TETNG PRELIMINARY; PRT; 414 AA.
AC QARKY3
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE Chromosome 1 SCAP15025, whole genome shotgun sequence. (Fragment).
GN ORFNames=gSTENG0032735001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygia; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_taxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallouf O., Aury J.-M., Brunet F., Pettit J.-L., Stange-Thomann N.,
RA Mauceli E., Aureau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RN the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SUBCELLULAR LOCATION: Membrane (By similarity).
CC -! SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CAAE01015025; CAG10949.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR003980; H3_rcpt.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
FT NON TER 414
FT SEQUENCE 414 AA; 46481 MW; 425E1F83C1DE28C4 CRC64;
Query Match 35.8%; Score 733.5; DB 2; Length 414;
Best Local Similarity 39.7%; Pred. No. 1.3e-44;
Matches 167; Conservative 60; Mismatches 129; Indels 65; Gaps 11;
Qy 1 MSESNTGILPPAA-----QVPLAFILMSFAFAIMVGNVAVILAFVVDRLNRHR 49
Db 5 MLESNSGNLTTPAVSEAGTALPGVLSVILSVLVVVVGNALVIAFVMDKLRNQ 64
Qy 50 SNYPFLNLAISDFLVGLISIPLYIPIHVLF-NWNFSGICMFWLITDYLLCTASVYVILI 108
Db 65 SNYPFLNLAISDFLVGLAFGAFIPVYPSLTGRRWMLGKGLCKVLMVMDYLLCSASFVILI 124
Qy 109 SYDRYQSVSNVSYRAQHTGIMKIVAOVAVVILAFVNGPMLIASDSW---KNSTNTKDC 166
Db 125 SYDRFLSVTRAVKYRVQRNMTRQAVLKQVAVVILAFVLPAILFWEAMVQSVVPPHEC 184
Qy 167 EPGFVTEWYVILITMLLEFLPLVISVAYFNVQIYMSLWKR-----RALSRC 212
Db 185 YAEFYFTWYLLSGSIFETFPFVSVAFNLISYILNHRRIKOGASGDDBARQGVSKK 244
Qy 213 PSHAGFTSTSSASGHLHRAGVACRTSNPGL-----KESAASSHSSPRKSKILSVLR 266
Db 245 PRDGVVTVF-----FMKTRKVC--SEPTAISAVIEDDEAPSHSSRDPNSSQLI--- 294
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various isoforms are mainly coexpressed in brain, but their relative expression level varies in a region-specific manner. Isoform 3 and isoform 7 are highly expressed in the thalamus, caudate nucleus and cerebellum while isoform 5 and isoform 6 show a poor expression. Isoform 5 and isoform 6 show a high expression in the amygdala, substantia nigra, cerebral cortex and hypothalamus. Isoform 7 is not found in hypothalamus or substantia nigra.

!- MISCELLANEOUS: Does not bind to cimetidine and triptolidine. Shows modest affinity for thiopramide, imetit, N-alpha-methylhistamine and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to idopropoxyfan while isoforms 1 and 3 bind it with high affinity.

!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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EMBL; AF140538; AAD38151.1; -; mRNA.  
 EMBL; AB045369; BAB20090.1; -; mRNA.  
 EMBL; AB019000; BAB17030.1; -; mRNA.  
 EMBL; AJ296652; CAC51025.1; -; Genomic\_DNA.  
 EMBL; AJ278250; CAC39434.1; -; Genomic\_DNA.  
 EMBL; AF363791; AAK50040.1; -; mRNA.  
 EMBL; AL078633; CAC04014.1; -; Genomic\_DNA.  
 EMBL; BC096840; AAH96840.1; -; mRNA.  
 EMBL; ENSG00000101180; Homo sapiens.  
 DR HGNC; HGNC:5184; HRH3.  
 DR MIM; 604525; gene.  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0005886; C: plasma membrane; TAS.  
 DR GO; GO:0004969; F: histamine receptor activity; TAS.  
 DR GO; GO:0007187; P: G-protein signaling, coupled to cyclic nucl. .; TAS.  
 DR GO; GO:0007269; P: neurotransmitter secretion; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR003980; H3 rcpt.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCR\_Rhodpsn.  
 DR PRINTS; PR01471; HISTAMINEHR3.  
 DR PROSITE; PS00237; G-PROTEIN RECP F1\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECP F1\_2; 1.  
 DR Alternative splicing; G-protein coupled receptor; Glycoprotein; Membrane; Polymorphism; Receptor; Transducer; Transmembrane.

CHAIN 1 445  
 Histamine H3 receptor.  
 /FTid=PRO\_0000069690.  
 FT TOPO\_DOM 1 39 Extracellular (Potential).  
 FT TRANSMEM 40 60 Potential.  
 FT TOPO\_DOM 61 70 Cytoplasmic (Potential).  
 FT TRANSMEM 71 91 Potential.  
 FT TOPO\_DOM 92 108 Extracellular (Potential).  
 FT TRANSMEM 109 129 Potential.  
 FT TOPO\_DOM 130 156 Cytoplasmic (Potential).  
 FT TRANSMEM 157 177 Potential.  
 FT TOPO\_DOM 178 196 Extracellular (Potential).  
 FT TRANSMEM 197 217 Potential.  
 FT TOPO\_DOM 218 359 Cytoplasmic (Potential).  
 FT TRANSMEM 360 380 Potential.  
 FT TOPO\_DOM 381 395 Extracellular (Potential).  
 FT TRANSMEM 396 416 Potential.  
 FT TOPO\_DOM 417 445 Cytoplasmic (Potential).  
 FT COMPBTAS 20 23 Poly-Ala.  
 FT COMPBTAS 250 256 Poly-Pro.  
 FT CARBOHYD 11 11 N-linked (GlcNAc.. ) (Potential).  
 FT VARSPPLIC 85 98 Missing (in isoform 4).  
 FT VARSPPLIC 197 315 Missing (in isoform 5).  
 FT CARBOHYD 227 342 Missing (in isoform 6).  
 FT VARSPPLIC 35.3%; Score 722.5; DB 1; Length 445;  
 Best Local Similarity 38.8%; Pred. No. 8.5e-44;  
 Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFIMSSFAFAMVGNVAVILAFVVDRLNLRHSYFFLNLAISDFVLGLIPIYIPHYL 77  
 DB 37 LAALMALIIVATVIGNALVLAFAVADSLRTQNNFFLLNLAISDFLVGAFCIPLVYPYVL 96  
 QY 78 F-NNFGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVSNVSYRAQHTGIMKIVAQM 136  
 DB 97 TGRWTFGRGLCKLWLVVDYLLCTSAFNVLISYDRFLSVTRVSYRAQOQDTRAVRKM 156  
 QY 137 VAVWILAFVNGPMILASDSWK-----NSTWKDCPEGFVTEWYILITMILEFLPLVIS 191  
 DB 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFPFPLS 213  
 QY 192 VAYFNVIY-----WSLWKRALSRCPSH 215  
 DB 214 VTFFNLIYLNIRTRRLDLGAREAAAGPEPPPAQSPPPPPCGWCQWKGHEAMPLH 273  
 QY 216 -----AGFSTTSSAGHLHRAGVACTSNPGLKESAAHSRSESPPRKSSILV 263  
 DB 274 RYGVGEAAVGAEGEATLGGGGG-----GSVASPTSSG-----SSRGTETPR 318  
 QY 264 SLRTHMNSSITAFKVGFSRSESAAALRQR-----EYAEELRGRKLARSLAILLSAF 314  
 DB 319 -----SLKRGSKPSASSASLEKRMKMWVSQSFQRPFLSRDRKVAKSLAVIVSIF 367  
 QY 315 AICWAPYCLFTIVLSTYPRTERPKSVVSYAFWLOWFNSFVNPLYPLCHRRFQKAFWKI 374  
 DB 368 GLCWAPYTLMLIIRAACHGCV-P-DYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426  
 QY 375 LCVTNK 379  
 DB 427 LCPOK 431

RESULT 12  
 Q548M6\_HUMAN PRELIMINARY; PRT; 445 AA.  
 AC Q548M6;  
 DT 24-MAY-2005, integrated into UniProtKB/TREMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 21-FEB-2006, entry version 10.  
 DE Histamine H3 receptor isoform 1.  
 GN Name=HRH3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Hippocampus;  
 RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,  
 Weiner D.M.;  
 RT "Molecular Cloning and Characterization of Functionally Distinct  
 RT Isoforms of the Human Histamine H3 Receptor.";  
 RL Neuropharmacology 0:0-0(2002).  
 CC !- SUBCELLULAR LOCATION: Membrane (By similarity).  
 CC !- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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EMBL; AF321910; AAL71911.1; -; mRNA.  
 DR Ensembl; ENSG00000101180; Homo sapiens.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0016020; C: membrane; IEA.  
 DR GO; GO:0004969; F: histamine receptor activity; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.  
 DR GO; GO:0007165; P: signal transduction; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR003980; H3\_rcpt.

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DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01471; HISTAMINEH3.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
  Transmembrane.
SQ SEQUENCE 445 AA; 48657 MW; 001205D765B705F5 CRC64;

Query Match          35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.5e-44;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFIMSSFAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHL 77
DB 37 LAALMALLIVATVIGNALVMAFVADSSLTQNNFFLLNLAISDFLVGFCIPLYVPL 96

QY 78 F-NNFSGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVNAVSVRAQHTGIMKIVAQM 136
DB 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQQQDTRAVRKM 156

QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPFGFTWYILITMLLEFLLPVIS 191
DB 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213

QY 192 VAYFNVQIY-----WSLWKRRALSRCPSH 215
DB 214 VTFNLSIYLNQIRTRFLRDGAREAGPPPEAQAQSPPPPGCGCWKGHGKAMPLH 273

QY 216 -----AGFSTSSASGHLHRAGVACRTSNPGLKESAAHSRSPRRKGSILV 263
DB 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSRGTGTERP----- 318

QY 264 SLRTHMNSSITAFKVGFWSESAALRQ-----EYAEILRGRKLARSAILLSAF 314
DB 319 -----SLKRGSKPSASSASLEKRMKMSQSFQRFSLSRDRKVAKSIAVVISIF 367

QY 315 AICWAPYCLFTIVLSTYPRTERPKSVWYSTAFWLQWNSFVNPFLYPLCHRRRQKAFWKI 374
DB 368 GLCWAPYTLMLIIRACHGCHVP-DYWTETFWLLMANSVNPVLYPLCHHSFRAPTKL 426

QY 375 LCVTK 379
DB 427 LCPQK 431

RESULT 13
ID_HRH3_CAVPO STANDARD; PRT; 445 AA.
AC Q9J135; Q9J136;
DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
DT 16-NOV-2001, sequence version 2.
DT 07-MAR-2006, entry version 32.
DE Histamine H3 receptor (HH3R).
GN Names=HH3;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS LONG AND SHORT).
RC TISSUE=Brain;
RX MEDLINE=20218440; PubMed=10757514;
RA Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C.,
RA Cochois V., Schwartz J.-C., Arrang J.-M.;
RT "Cloning and cerebral expression of the guinea pig histamine H3
RT receptor: evidence for two isoforms.";
RL NeuroReport 11:755-759(2000).
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylylate cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of
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agonist).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long; Synonyms=H3L;
CC Name=Short; Synonyms=H3S;
CC IsoId=Q9J135-1; Sequence=Displayed;
CC IsoId=Q9J135-2; Sequence=VSP_001880;
CC -!- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the
CC brain. Highly expressed in discrete neuronal populations such as
CC pyramidal cells in cerebral cortex or cerebellar Purkinje cells.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AF267537; AAF78947.1; -; mRNA.
CC EMBL; AF267538; AAF78950.1; -; mRNA.
CC InterPro; IPR000276; GPCR_Rhodpan.
CC DR InterPro; IPR003980; H3_rcpt.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PRINTS; PR01471; HISTAMINEH3.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
  Membrane; Receptor; Transducer; Transmembrane.
KW Histamine H3 receptor.
FT CHAIN 1 445 /FTID=PRO_0000089689.
FT TOPO_DOM 1 40 Extracellular (Potential).
FT TRANSMEM 41 61 Potential.
FT TOPO_DOM 62 71 Cytoplasmic (Potential).
FT TRANSMEM 72 92 Potential.
FT TOPO_DOM 93 109 Extracellular (Potential).
FT TRANSMEM 110 130 Potential.
FT TOPO_DOM 131 157 Cytoplasmic (Potential).
FT TRANSMEM 158 178 Potential.
FT TOPO_DOM 179 197 Extracellular (Potential).
FT TRANSMEM 198 218 Potential.
FT TOPO_DOM 219 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Potential.
FT TOPO_DOM 381 398 Extracellular (Potential).
FT TRANSMEM 399 419 Potential.
FT TOPO_DOM 420 445 Cytoplasmic (Potential).
FT COMBIAS 20 24 Poly-Ala.
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 276 305 Missing (in isoform Short).
FT FTID=VSP_001880.
FT SEQUENCE 445 AA; 48735 MW; BAE206A3887189A0 CRC64;

Query Match          35.2%; Score 721; DB 1; Length 445;
Best Local Similarity 39.8%; Pred. No. 1.1e-43;
Matches 162; Conservative 54; Mismatches 133; Indels 58; Gaps 9;

QY 18 LAFIMSSFAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHL 77
DB 38 LAALMALLIVATVIGNALVMAFVADSSLTQNNFFLLNLAISDFLVGFCIPLYVPL 97

QY 78 F-NNFSGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVNAVSVRAQHTGIMKIVAQM 136
DB 98 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQQQDTRAVRKM 157

QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPFGFTWYILITMLLEFLLPVIS 191
DB 158 VLWVWLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 214

QY 192 VAYFNVQIY-----WSLWKRRALSRCPS 214
DB 215 VTFNLSIYLNQIRTRFLRDGAREAGDPPLPEAQSSPPPPPGCGCWKPGKGESMPL 274

QY 215 HA-GFSTTSSSA-SGHLHRAGVACRTSNPGLKESAAHSRSPRRKGSILVSLRTHMNSS 272
DB 275 HRYGVGEAGPGAAGEAALGGGSAASPTSSGSSSRGTGTERP-----SLKRGSKPS 327
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Qy 273 ITAPKVGSPWRSSEAAALRORBYAELLRGRKLARSALAILLSAFALCWAPYCLFTIVLSTYP 332
Db 328 ASSASLEKRMKMSQSIQR--FLSRDRKKVAKSLAIVSIFGLCWAPYTLMIIRAACH 385
Qy 333 RTERPKSVWTSIAFWLQWNSFVNPELYPLCHRRFQKAFWKILCVTK 379
Db 386 GHCVP-DYWTETSWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQK 431

RESULT 14
Q865E1 MACMU
ID Q865E1 MACMU PRELIMINARY; PRT; 445 AA.
AC Q865E1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 21-FEB-2006, entry version 15.
DE Histamine receptor H3.
GN Name=HRH3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP Rattus norvegicus (Rat).
RA Yao B.B., Sharma R., Cassar S., Esbenshade T.A., Hancock A.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
EMBL: AY231164; AAC63757.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004969; F:histamine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003980; H3_rept.
DR Pfam: PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 445 AA; 48591 MW; E79440A4EC09CA8C CRC64;

Query Match 35.18; Score 718.5; DB 2; Length 445;
Best Local Similarity 38.78; Pred. No. 1.7e-43;
Matches 163; Conservative 52; Mismatches 121; Indels 85; Gaps 9;

Qy 18 LAFIMSFSAFIMVGNVAVILAFVVDNLRHRSNYFFLNLAISDFVLGLISIPLYPHVL 77
Db 37 LAALMALLIVATVIGNALVWALFVADSSLRTONNFFLNLAISDFLVGACPIPLYPVYL 96

Qy 78 F-NWFGSGICMFWLITDYLLCTASVYNVILSYDRYQSVNAVSYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLKLVWVYLLCTSSAFNVILSYDRFLSVTRAVSYRAQGNTRAVRKM 156

Qy 137 VAWVILAFVNGPMLASDSWK-----NSTNTKDCBGFVTEWYLTITMLLFFLPVIS 191
Db 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPGHCYAEFFNYFNWYFLITASTLEFFTPFLS 213

Qy 192 VAFNVQVY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYINQRTLRLDGAREAGGPPPPPAQSPPPPPCGCWCQKQHGHEAMPLH 273

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Qy 216 -----AGFTSTSSASGHLHRAGVACRTSNPGLKESAAHSSESPPRKSSILVLSRT 267
Db 274 RYGVGEAAAAGAEATALGGGGGSAASPTSSG-----SSSRGTERPR----- 318
Qy 268 HNSSTAFAPKVGSPWRSSEAAALROR-----EYAEELLRGRKLARSALAILLSAFALCW 318
Db 319 -----SLKRGSKPSASASLEKRMKMSQSFQRLSRDRKVKAKSLAIVSIFGLCW 371
Qy 319 APYCLFTIVLSTYPTRERPKSVWTSIAFWLQWNSFVNPELYPLCHRRFQKAFWKILCVT 378
Db 372 APYTLMIIRAACHGHCVP-DYWTETSWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQ 430
Qy 379 K 379
Db 431 K 431

RESULT 15
HRH3 RAT
ID -HRH3 RAT STANDARD; PRT; 445 AA.
AC Q8QYN8; Q8QYN6; Q8QYN7; Q8QYN9;
DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-2000, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Histamine H3 receptor (HRH3).
GN Name=Hrh3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP Nucleotide sequence [mRNA] (ISOFORM 1).
RC TISSUE=Hypothalamus;
RX MEDLINE=20330707; PubMed=10869375;
RA Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
RT "Cloning of rat histamine H3 receptor reveals distinct species
RT pharmacological profiles.";
RL J. Pharmacol. Exp. Ther. 293:771-778 (2000).
RN [2]
RP Nucleotide sequence [mRNA] (ISOFORMS 1 AND 2).
RC TISSUE=Corpus striatum;
RX MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
RA Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
RA Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
RT "High constitutive activity of native H3 receptors regulates histamine
RT neurons in brain.";
RL Nature 408:860-864 (2000).
RN [3]
RP Nucleotide sequence [mRNA] (ISOFORMS 1; 2; 3 AND 4).
RA Itadani H., Takimura T., Nakamura T., Ohta M.;
RT "Cloning of a novel G protein-coupled receptor.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=99278519; PubMed=10347254;
RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
RA Huvvar A., Jackson M.R., Erlander M.G.;
RT "Cloning and functional expression of the human histamine H3
RT receptor.";
RL Mol. Pharmacol. 55:1101-1107 (1999).
CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylylate cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of
CC agonist).
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=H3L;
CC IsoId=Q8QYN8-1; Sequence=Displayed;
CC Name=2; Synonyms=H3S;

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CC IsoId=Q9QYN8-2; Sequence=VSP_001887;
CC Name=3;
CC IsoId=Q9QYN8-3; Sequence=VSP_001888;
CC Name=4;
CC IsoId=Q9QYN8-4; Sequence=VSP_001888, VSP_001889;
CC -1- TISSUE SPECIFICITY: Expressed abundantly in brain, most notably
CC throughout the thalamus, the ventromedial hypothalamus and the
CC caudate nucleus. Isoform 1 is largely predominant in all tissues.
CC -1- MISCELLANEOUS: Proxifan acts as a potent neutral antagonist while
CC thioetheramide, ciproxifan and FUB465 act as potent inverse
CC agonists.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC ENBL; AF237919; AAF82086.1; -; mRNA.
CC ENBL; AY009370; AAK02069.1; -; mRNA.
CC ENBL; AB015646; BAA88765.1; -; mRNA.
CC ENBL; AB015646; BAA88766.1; -; mRNA.
CC ENBL; AB015646; BAA88767.1; -; mRNA.
CC ENBL; AB015646; BAA88768.1; -; mRNA.
CC Ensembl; ENSRNOG0000008080; Rattus norvegicus.
CC RGD; 620630; Hrh3.
CC GO; GO:0004969; F:histamine receptor activity; IDA.
CC GO; GO:0007194; P:negative regulation of adenylate cyclase ac. .; IDA.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR003980; H3_rcpt.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR01471; HISTAMINEH3R.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW Membrane; Receptor; Transducer; Transmembrane.
CC CHAIN 1 445
FT FT 1 39 Extracellular (Potential).
FT FT 40 60 Potential.
FT FT 61 70 Cytoplasmic (Potential).
FT FT 71 91 Potential.
FT FT 92 108 Extracellular (Potential).
FT FT 109 129 Potential.
FT FT 130 156 Cytoplasmic (Potential).
FT FT 157 177 Potential.
FT FT 178 196 Extracellular (Potential).
FT FT 197 217 Potential.
FT FT 218 359 Cytoplasmic (Potential).
FT FT 360 380 Potential.
FT FT 381 396 Extracellular (Potential).
FT FT 397 417 Potential.
FT FT 418 445 Cytoplasmic (Potential).
FT FT 446 446 Poly-Ala.
FT FT 447 447 N-linked (GlcNAc.. ) (Potential).
FT FT 448 448 Missing (in isoform 3 and isoform 4).
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FT FT 450 450 Missing (in isoform 2).
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FT FT 453 VQPHGSLQOCWK -> CVERLGKLEASLLPLWMFSGRWR
FT FT 454 RKVCELDVPMFNOERQNCRGARWIGRCGLPRPPSVLQ
FT FT 455 LPAEPRQLLPAPPPGLGRWPCPACVCTIRINGWVMG
FT FT 456 (in isoform 4).
FT FT 457 457 /FTid=VSP_001889.
FT FT 458 458 SEQUENCE 445 AA; 48588 MW; 63DFEFC21758FESB CRC64;
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GenCore version 5.1.8  
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Run on: May 24, 2006, 13:34:45 ; Search time 29 Seconds  
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1180.154 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKWALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC\_Celerra\_SID3S/protdata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SID3S/protdata/2/iaa/7\_COMB.pep.\*
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- 5: /EMC\_Celerra\_SID3S/protdata/2/iaa/PGTUS COMB.pep.\*
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- 7: /EMC\_Celerra\_SID3S/protdata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1370.5	66.9	390	2	US-09-414-010-2
2	1370.5	66.9	390	2	US-09-812-216-2
3	1370.5	66.9	390	2	US-09-875-076-14
4	722.5	35.3	445	1	US-08-985-090-2
5	722.5	35.3	445	2	US-09-165-543-2
6	722.5	35.3	445	2	US-09-167-354-7
7	722.5	35.3	445	2	US-09-642-855-7
8	722.5	35.3	445	2	US-09-642-514-7
9	722.5	35.3	445	2	US-09-642-852-7
10	722.5	35.3	445	2	US-10-453-106-1
11	722.5	35.3	445	2	US-09-949-016-10930
12	722.5	35.3	453	2	US-09-891-053-20
13	718.5	35.1	445	2	US-10-453-106-2
14	718.5	35.0	445	2	US-09-165-543-5
15	716.5	35.0	445	2	US-09-891-053-25
16	716.5	35.0	445	2	US-10-453-106-3
17	709.5	34.6	413	2	US-09-891-053-1
18	621.5	30.3	351	1	US-09-524-162-2
19	582.5	28.4	362	1	US-08-985-090-5
20	582.5	28.4	362	2	US-09-165-543-32
21	427	20.8	348	1	US-08-118-270-13
22	427	20.8	348	5	PCT-US93-08528-13
23	427	20.8	355	1	US-08-118-270-11
24	427	20.8	355	5	PCT-US93-08528-11
25	415.5	20.3	479	1	US-08-313-553-7
26	415.5	20.3	479	2	US-08-767-993-7

27	408	19.9	460	2	US-09-826-509-513	Sequence 513, App
28	402.5	19.7	590	2	US-09-538-092-367	Sequence 967, App
29	399.5	19.5	532	2	US-09-826-509-521	Sequence 521, App
30	397.5	19.4	590	2	US-09-826-509-517	Sequence 517, App
31	393	19.2	354	1	US-08-313-853-9	Sequence 9, Appli
32	393	19.2	354	2	US-08-767-993-9	Sequence 9, Appli
33	390.5	19.1	501	1	US-08-722-001-14	Sequence 14, Appli
34	390.5	19.1	501	1	US-08-467-568-9	Sequence 9, Appli
35	390.5	19.1	501	1	US-09-030-582-9	Sequence 9, Appli
36	389.5	19.0	513	1	US-08-406-855A-21	Sequence 21, Appli
37	389.5	19.0	513	2	US-09-206-899-21	Sequence 21, Appli
38	389.5	19.0	515	1	US-08-444-734A-7	Sequence 7, Appli
39	389.5	19.0	515	1	US-08-406-855A-22	Sequence 22, Appli
40	389.5	19.0	515	2	US-09-206-899-22	Sequence 22, Appli
41	388.5	19.0	400	2	US-09-826-509-491	Sequence 491, App
42	388.5	19.0	572	1	US-08-334-698-2	Sequence 2, Appli
43	388.5	19.0	572	1	US-08-228-932-2	Sequence 2, Appli
44	388.5	19.0	572	1	US-08-468-919-2	Sequence 2, Appli
45	388.5	19.0	572	1	US-08-722-001-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1  
US-09-414-010-2  
; Sequence 2, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsema, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; NUMBER FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-414-010-2

Query Match	66.9%	Score 1370.5;	DB 2;	Length 390;
Best Local Similarity	68.1%	Pred. No. 2e+105;		
Matches 267;	Conservative 40;	Mismatches 82;	Indels 3;	Gaps 2;
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Db	1	MPDTNSTINLSLSTRVTLAFMSLVAFIMGNALVILAFVVDKRLHRSSYFFLNLAIS	60	
Qy	61	DFLVGLISIPLYIPHLVFNFGSGICMFWLITDYLCTASVYNNIVLISYDRYSQSVNAV	120	
Db	61	DFVGVVISIPLYIPHTLTFENDFGKEICVFWLITDYLCTASVYNNIVLISYDRYSQSVNAV	120	
Qy	121	SYRAQHTGIMKIQAQVAVILAFVNGPMILASDSWKNSTNTKDCPCGFTWWTILIT	180	
Db	121	SYRTQHTGVILKIVTLAVAVVILAFVNGPMILVSESWKDEGS--ECEPGFTSEWYILAIT	178	
Qy	181	MLLEFLAPVLSVAFVNOIVKSLMKRRALSRCPHAGFTSTSSASGHLHAGVACRTSN	240	
Db	179	SFLFVPIVILVAFVNNIIVSLMKRDLHRCQHPGLTAVSSNICGHSFGRISRRSL	238	
Qy	241	PGLKESAAARHSESPPRKSSILVSLRTHMNSITAFKVGSPWRSESAALRQREYAEILRG	300	
Db	239	SASTEVPAFHSERQRRKSSILMFSSRTKNSNTASKMGSPSQSDSVALHQREHVELLRA	298	
Qy	301	RKLARSAILLSAPAIQWAPCYCLFTIVLSTYPTPTPKSVWVYSIAFWLQWNSFVNPLY	360	

Db 299 RRLAKSLAIIIGVAVCWAPYSLFTIVLSFYSSATGPKSVYVIAFWLQWFSVFNPLLY 358  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 390

## RESULT 2

US-09-812-216-2  
; Sequence 2, Application US/09812216  
; Patent No. 6613533  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/812,216  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09/414,010  
; PRIOR FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-812-216-2

Query Match 66.9%; Score 1370.5; DB 2; Length 390;

Best Local Similarity 68.1%; Pred. No. 2e-105;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSESNSGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNLRHRSNYFFLNLAIS 60  
Db 1 MPDTNSTINLSLSTRVTLAFMSLVAFALMGNALVILAFVVDKRLHRSNYFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPIHVLNFWNFGSGICMFWLITDYLCTASVNVNIVLSYDRYQSVSNV 120  
Db 61 DFFVGVISIPLYIPIHVLNFWNFGSGICMFWLITDYLCTASVNVNIVLSYDRYQSVSNV 120  
Qy 121 SYRAQHTGIMKIQAQVAVMILAFVNGPMLASDSWKNSTNTKDCBPGFVTEWYILIT 180  
Db 121 SYRTQHTGVLKIVLTMVAVVILAFVNGPMLVSESWKDEGS--ECEPGFFSEWYILIT 178  
Qy 181 MLLEFLLPVLSVAVFNVQIYWSLWKRALSRCPHAGFTSTSSASGHLHRAQVACRTSN 240  
Db 179 SFLEFVPIVILVAVFNNWVWSLWKRLHRCQHPGLTAVSSNICGHSFRGLSSRSL 238  
Qy 241 PGLKESAAHRHSESPRKSSILVSLRTHMSSITAFKVGFSFWRSESAAALRQREYAEILRG 300  
Db 239 SASTEVPAFSEHSEQRKSSLMFSRTKMSNTTASKMGFSQSDSVALLHQREHVELLRA 298  
Qy 301 RKLARSLAIIISAPAIWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFSVFNPLLY 360  
Db 299 RRLAKSLAIIIGVAVCWAPYSLFTIVLSFYSSATGPKSVYVIAFWLQWFSVFNPLLY 358  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 390

## RESULT 3

US-09-875-076-14  
; Sequence 14, Application US/09875076  
; Patent No. 6869776  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping

; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
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; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-875-076-14

Query Match 66.9%; Score 1370.5; DB 2; Length 390;

Best Local Similarity 68.1%; Pred. No. 2e-105;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSESNSGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNLRHRSNYFFLNLAIS 60  
Db 1 MPDTNSTINLSLSTRVTLAFMSLVAFALMGNALVILAFVVDKRLHRSNYFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPIHVLNFWNFGSGICMFWLITDYLCTASVNVNIVLSYDRYQSVSNV 120  
Db 61 DFFVGVISIPLYIPIHVLNFWNFGSGICMFWLITDYLCTASVNVNIVLSYDRYQSVSNV 120  
Qy 121 SYRAQHTGIMKIQAQVAVMILAFVNGPMLASDSWKNSTNTKDCBPGFVTEWYILIT 180  
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QY 181 MLEFLLPVISVAVNQIYWSLWKRALSRCPHAGSTTSSASGHLHRAGVACRTSN 240
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QY 241 PGLKESAAHSRHSPPRKSSILVSLRTHMNSSITAFKVGSEFWRSSESAALROREYAEALLRG 300
Db 239 SASTEVPAFHSERQRRKSSLMFSRTYMSNTTASRWGFSQSDSVALLHQREHVELLRA 298
QY 301 RKLARSAILLSAPAIWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWPNFSVNPFLY 360
Db 299 RRLAKSLAILLGVPAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWPNFSVNPFLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 390

RESULT 4
US-08-985-090-2
; Sequence 2, Application US/08985090
; Patent No. 5885693
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-2

Query Match 35.3%; Score 722.5; DB 1; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSFAPAIMVGNVILAFVDRNLHRNRYFFLNLAISDFLVGLISIPLYIPHVL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSSLTQNNFFLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NNFGSGICMFWLITDYLCTASVYNIIVLSYDRYQSVSNVSYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQOGDTRRAVRKM 156
QY 137 VAWNLAFLVNGPWILASDSWK-----NSNTKDCSPGFVTEWYILTITMLLEFLPVIS 191
Db 157 LLVWVLAFLLYGPAILL---SWEYLSGSGSIPEGHCVAFPFYNNYFLITASTLEFFTPFLS 213
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QY 192 VAYFNVOIY-----WSLWKRALSRCPSPH 215
Db 214 VTFENLSIYLNIRRLDGLAREAAAGBPPEAQPSPPPPCGCGKQKGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACHTSNPGLKESAAHSRHSPPRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG-----GSVASPTSSG-----SSSRGTERPR 318
QY 264 SLRTHMNSSITAFKVGSEFWRSSESAALRQ-----EVAELLRGRKLARSAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKMWVSQSTQRFRLSRDRKVAKSLAVIVSIF 367
QY 315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWPNFSVNPFLYPLCHRRFRFOKAFWKI 374
Db 368 GLCWAPYTLMLIIRAACHGCV-P-DYWYETSWLLWANSVNPVLYPLCHHSFRFAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 5
US-09-165-543-2
; Sequence 2, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-2

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSFAPAIMVGNVILAFVDRNLHRNRYFFLNLAISDFLVGLISIPLYIPHVL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSSLTQNNFFLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NNFGSGICMFWLITDYLCTASVYNIIVLSYDRYQSVSNVSYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQOGDTRRAVRKM 156
QY 137 VAWNLAFLVNGPWILASDSWK-----NSNTKDCSPGFVTEWYILTITMLLEFLPVIS 191
Db 157 LLVWVLAFLLYGPAILL---SWEYLSGSGSIPEGHCVAFPFYNNYFLITASTLEFFTPFLS 213
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Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSGSIPEGHCAEFYNNYFLITASTLEFFTPFLS 213
QY 192 VAYFNVOIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLIQRTRLRLDGAAREAGPEPPPEAQPSPPPPGCGWQKQHGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRHSPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAE LLRGRKLAARSAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKMWVSQSFQFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLWNSFVNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 6
US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-167-354-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSPAFAIMVGNVILAFVDRNLHRSNYFNLAIISDFLVGLISILYIYPHVL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSSLRQNNFFLLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NNFSGGICMFWLITDYLLCTASVNVNVLISYDRYQSVSNVAVSRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSGSIPEGHCAEFYNNYFLITASTLEFFTPFLS 213
QY 192 VAYFNVOIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLIQRTRLRLDGAAREAGPEPPPEAQPSPPPPGCGWQKQHGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRHSPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAE LLRGRKLAARSAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKMWVSQSFQFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLWNSFVNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 7
US-09-642-855-7
; Sequence 7, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-642-855-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSPAFAIMVGNVILAFVDRNLHRSNYFNLAIISDFLVGLISILYIYPHVL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSSLRQNNFFLLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NNFSGGICMFWLITDYLLCTASVNVNVLISYDRYQSVSNVAVSRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSGSIPEGHCAEFYNNYFLITASTLEFFTPFLS 213
QY 192 VAYFNVOIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLIQRTRLRLDGAAREAGPEPPPEAQPSPPPPGCGWQKQHGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRHSPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAE LLRGRKLAARSAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKMWVSQSFQFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLWNSFVNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426
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Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSGSIPEGHCAEFYNNYFLITASTLEFFTPFLS 213
QY 192 VAYFNVOIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLIQRTRLRLDGAAREAGPEPPPEAQPSPPPPGCGWQKQHGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRHSPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAE LLRGRKLAARSAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKMWVSQSFQFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLWNSFVNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 6
US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-167-354-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSPAFAIMVGNVILAFVDRNLHRSNYFNLAIISDFLVGLISILYIYPHVL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSSLRQNNFFLLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NNFSGGICMFWLITDYLLCTASVNVNVLISYDRYQSVSNVAVSRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSGSIPEGHCAEFYNNYFLITASTLEFFTPFLS 213
QY 192 VAYFNVOIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLIQRTRLRLDGAAREAGPEPPPEAQPSPPPPGCGWQKQHGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRHSPRRKSSILV 263
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Qy 375 LCVTK 379  
Db 427 LCPQK 431

## RESULT 8

US-09-642-514-7  
; Sequence 7, Application US/09642514  
; Patent No. 6437100

## ; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Erlander, Mark

; APPLICANT: Pyati, Jayashree

; APPLICANT: Huvar, Arne

; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

; FILE REFERENCE: ORT1290

; CURRENT APPLICATION NUMBER: US/09/642,514

; CURRENT FILING DATE: 2000-08-21

; PRIOR APPLICATION NUMBER: US 09/167,354

; PRIOR FILING DATE: 1998-10-06

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 445

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE

US-09-642-514-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;

Best Local Similarity 38.8%; Pred. No. 8.8e-52;

Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

Qy 18 LAFMLSSFAFALMGVAVVLAFLVVDRLNRHRSYFFLNLAISDFVLGLISIPLYIPHL 77

Db 37 LAALMALLIVATVLGNALVMLAFVADSSLRQTQNNFFLNLAISDFLVGAFICPLYVPVL 96

Qy 78 F-NNFGSGICMFWLITDYLCTASVNVILISYDRVQSVNAVSYRAQHTGIMKIVAQM 136

Db 97 TGRWTFGRGLCKLWLVVDYLLCTSAFNIVLISYDRFLSVTRAVSYRAQOQDTRAVRKM 156

Qy 137 VAVWILAFVNGPMLASDSWK-----NSTWTKDCEPGFVTEWYILITITMLLEFLLPVIS 191

Db 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213

Qy 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215

Db 214 VTFFNLSTIYLNIQRRRLRLDGAEEAGPEPPEAQPSPPPPGCWQKGHEAMPLH 273

Qy 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHSRHSPPRKSILV 263

Db 274 RYGVGEAAVGAEEAGTLGGGGG---GSVASPTSSG---SSSRGTERPR----- 318

Qy 264 SLRTHMNSSITAFKVGSPWRSSEALRQ-----EYAEALLRGRKLARSAILLSAF 314

Db 319 -----SLKRGSKPSASSASLEKRMKWSQSFTQRFRLSRDRKVAKSLAVIVSIF 367

Qy 315 AICWAPYCLFTIVLSTYPTERTPKSVVYSIAFWLQWFNFSFVNPFLYPLCHRRFQKAFWKI 374

Db 368 GLCWAPYTLMIIRAACHGHCVP-DYWTYETSWLLWANSVNPVLYPLCHHSFRFAFTKL 426

Qy 375 LCVTK 379

Db 427 LCPQK 431

## RESULT 9

US-09-642-952-7

; Sequence 7, Application US/09642852

; Patent No. 6855560

## ; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Erlander, Mark

; APPLICANT: Pyati, Jayashree

; APPLICANT: Huvar, Arne

; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

; FILE REFERENCE: SUBTYPE

; CURRENT APPLICATION NUMBER: US/09/642,852

; CURRENT FILING DATE: 2000-08-21

; PRIOR APPLICATION NUMBER: 09/167,354

; PRIOR FILING DATE: 1998-10-07

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 445

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE

US-09-642-852-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;

Best Local Similarity 38.8%; Pred. No. 8.8e-52;

Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

Qy 18 LAFMLSSFAFALMGVAVVLAFLVVDRLNRHRSYFFLNLAISDFVLGLISIPLYIPHL 77

Db 37 LAALMALLIVATVLGNALVMLAFVADSSLRQTQNNFFLNLAISDFLVGAFICPLYVPVL 96

Qy 78 F-NNFGSGICMFWLITDYLCTASVNVILISYDRVQSVNAVSYRAQHTGIMKIVAQM 136

Db 97 TGRWTFGRGLCKLWLVVDYLLCTSAFNIVLISYDRFLSVTRAVSYRAQOQDTRAVRKM 156

Qy 137 VAVWILAFVNGPMLASDSWK-----NSTWTKDCEPGFVTEWYILITITMLLEFLLPVIS 191

Db 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213

Qy 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215

Db 214 VTFFNLSTIYLNIQRRRLRLDGAEEAGPEPPEAQPSPPPPGCWQKGHEAMPLH 273

Qy 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHSRHSPPRKSILV 263

Db 274 RYGVGEAAVGAEEAGTLGGGGG---GSVASPTSSG---SSSRGTERPR----- 318

Qy 264 SLRTHMNSSITAFKVGSPWRSSEALRQ-----EYAEALLRGRKLARSAILLSAF 314

Db 319 -----SLKRGSKPSASSASLEKRMKWSQSFTQRFRLSRDRKVAKSLAVIVSIF 367

Qy 315 AICWAPYCLFTIVLSTYPTERTPKSVVYSIAFWLQWFNFSFVNPFLYPLCHRRFQKAFWKI 374

Db 368 GLCWAPYTLMIIRAACHGHCVP-DYWTYETSWLLWANSVNPVLYPLCHHSFRFAFTKL 426

Qy 375 LCVTK 379

Db 427 LCPQK 431

## RESULT 10

US-10-453-106-1

; Sequence 1, Application US/10453106

; Patent No. 6906060

; GENERAL INFORMATION:

; APPLICANT: Peschke, Bernd

; APPLICANT: Hohlweg, Rolf

; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPIRROLO[1,2-A]PYRAZINES,

; TITLE OF INVENTION: OCTAHYDROPIRDO[1,2-A]PYRAZINES AND

; TITLE OF INVENTION: DECAHYDROPIRAZINO[1,2-A]AZEPINES

; FILE REFERENCE: 6483.200-US

; CURRENT APPLICATION NUMBER: US/10/453,106

; CURRENT FILING DATE: 2003-06-03

; PRIOR APPLICATION NUMBER: US 60/387,047

Query Match 35.3%; Score 722.5; DB 2; Length 445;  
Best Local Similarity 38.8%; Pred. No. 8.8e-52;  
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;  
PRIORITY FILING DATE: 2002-06-07  
PRIORITY APPLICATION NUMBER: Danish Application no. PA 2002 00863  
PRIORITY FILING DATE: 2002-06-06  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 445  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-453-106-1

Query Match 35.3%; Score 722.5; DB 2; Length 445;  
Best Local Similarity 38.8%; Pred. No. 8.8e-52;  
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;  
QY 18 LAFLMSSFAFAMVGNVAVILAFVVDNRNLHRNSYFFLNLAISDFLVGLISIPLYIPHVL 77  
DB 37 LAALMALLIVATVIGNALVNLAFVADSSLRTONNFFLLNLAIISDFLVGAFCIPLYIPYVL 96  
QY 78 F-NWNFGSGICMEFWLITDYLLCTASVYVNIIVLISYDRYQSVNAVSVYRAQHTGIMKIVAQM 136  
DB 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSVYRAQOGDTRRAVRKM 156  
QY 137 VAVWILAFVNGPMILASDSWK-----NSNTWKDCPEGFVTEWVILITMLLEPFLPVIS 191  
DB 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPGEGHCAEFFYNNVFLITASTLEFFFTPLS 213  
QY 192 VAVENVOIY-----WSLWKRRALSRCPSH 215  
DB 214 VTFNLSIYLNIOQRTRLRDLGAREAGPPEPPPEAQPSPPPPGCGWCQKQGHGEMPLH 273  
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRSHSPRRKSSILV 263  
DB 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSSRGTERPR----- 318  
QY 264 SLRTHMNSSITAPKVGFWRSSESAALRQ-----EYAEALLRGRKLARSAILLSAF 314  
DB 319 -----SLKRGSKPSASSASLEKRMKMSQSFTQRFRLSRDRKVAKSLAVIVSIF 367  
QY 315 AICWAPYCLFTIVLSTVPRTERPKSVWYSYAFWLOWNSFVNPFLYPLCHRRRFOKAFWKI 374  
DB 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSWLLWANSVNPVLYPLCHHSFRRAFTKL 426  
QY 375 LCVTK 379  
DB 427 LCPQK 431

RESULT 11  
US-09-949-016-10930  
; Sequence 10930, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10930  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10930

Query Match 35.3%; Score 722.5; DB 2; Length 449;  
Best Local Similarity 38.8%; Pred. No. 8.9e-52;  
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;  
QY 18 LAFLMSSFAFAMVGNVAVILAFVVDNRNLHRNSYFFLNLAISDFLVGLISIPLYIPHVL 77  
DB 41 LAALMALLIVATVIGNALVNLAFVADSSLRTONNFFLLNLAIISDFLVGAFCIPLYIPYVL 100  
QY 78 F-NWNFGSGICMEFWLITDYLLCTASVYVNIIVLISYDRYQSVNAVSVYRAQHTGIMKIVAQM 136  
DB 101 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSVYRAQOGDTRRAVRKM 160  
QY 137 VAVWILAFVNGPMILASDSWK-----NSNTWKDCPEGFVTEWVILITMLLEPFLPVIS 191  
DB 161 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPGEGHCAEFFYNNVFLITASTLEFFFTPLS 217  
QY 192 VAVENVOIY-----WSLWKRRALSRCPSH 215  
DB 218 VTFNLSIYLNIOQRTRLRDLGAREAGPPEPPPEAQPSPPPPGCGWCQKQGHGEMPLH 277  
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRSHSPRRKSSILV 263  
DB 278 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSSRGTERPR----- 322  
QY 264 SLRTHMNSSITAPKVGFWRSSESAALRQ-----EYAEALLRGRKLARSAILLSAF 314  
DB 323 -----SLKRGSKPSASSASLEKRMKMSQSFTQRFRLSRDRKVAKSLAVIVSIF 371  
QY 315 AICWAPYCLFTIVLSTVPRTERPKSVWYSYAFWLOWNSFVNPFLYPLCHRRRFOKAFWKI 374  
DB 372 GLCWAPYTLMIIRAACHGCHVP-DYWYETSWLLWANSVNPVLYPLCHHSFRRAFTKL 430  
QY 375 LCVTK 379  
DB 431 LCPQK 435

RESULT 12  
US-09-891-053-20  
; Sequence 20, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takamura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
; FILE REFERENCE: 06501-083001  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-891-053-20

Query Match 35.3%; Score 722.5; DB 2; Length 453;  
Best Local Similarity 38.8%; Pred. No. 9e-52;  
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;  
QY 18 LAFLMSSFAFAMVGNVAVILAFVVDNRNLHRNSYFFLNLAISDFLVGLISIPLYIPHVL 77



Db 37 LAALMALLIVATVGNALVLAFAVDSSLRQNNFFLNLAISDFLVGAFCIPLYVPVL 96  
Qy 78 F-NWNFGSGICMFWLITDYLLCTASVYVNLISYDRYQSVNAVSYRAQHTGIMKIYAQM 136  
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQOQDTRAVRKM 156  
Qy 137 VAVWILAFVNGPMLASDSWK-----NSTNTKDCPEGFVTEWYILITITMLLEFLLPVIS 191  
Db 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTFPLS 213  
Qy 192 VAYFNVOIY-----WSLWKRRALSRCPSH 215  
Db 214 VTFNLSIYLNIOQRRLRLDCAEAGPEPPPEAQPSPPPPCGCMGCKQKHGSEAMPLH 273  
Qy 216 -----AGSTTSSASGHLHRAAGVACRTSNPGLKESAAASRHSESPRRKSSILV 263  
Db 274 RYGVGEAAVGAEGATELGGGGG-----GSVASPTSSG-----SSSRGTERPR----- 318  
Qy 264 SLRTHMNSSITAFKVGFWRSSESALRQ-----EYAEALLRGRKLARSLLAISAF 314  
Db 319 -----SLRKGSKPSASSASLEKRMKMWVSQFTQRFRLSRDRKVAKSLAVISIF 367  
Qy 315 AICWAPYCLFTIVLSTYRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKI 374  
Db 368 GLCWAPYLLMIIRAACHGCHVP-DYWTYETSWLLWANSVNPVLYPLCHHSFRRAFTKL 426  
Qy 375 LCVTK 379  
Db 427 LCPQK 431

## RESULT 13

US-10-453-106-2  
; Sequence 2, Application US/104531106  
; Patent No. 6906060  
; GENERAL INFORMATION:  
; APPLICANT: Peschke, Bernd  
; APPLICANT: Hohlweg, Rolf  
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPIRROLO [1,2-a] PYRAZINES,  
; TITLE OF INVENTION: OCTAHYDROPIRIDO [1,2-a] PYRAZINES AND  
; TITLE OF INVENTION: DECAHYDROPIRAZINO [1,2-a] AZEPINES  
; FILE REFERENCE: 6483.200-US  
; CURRENT APPLICATION NUMBER: US/10/453.106  
; CURRENT FILING DATE: 2003-06-03  
; PRIOR APPLICATION NUMBER: US 60/387,047  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863  
; PRIOR FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Monkey  
US-10-453-106-2

Query Match 35.1%; Score 718.5; DB 2; Length 445;  
Best Local Similarity 38.7%; Pred. No. 1.9e-51;  
Matches 163; Conservative 52; Mismatches 121; Indels 85; Gaps 9;

Qy 18 LAFIMSSFAFIMVGNNAVILAFVVDNRNLRHSRYFFLNLAISDFLVGLISIPLYIPHL 77  
Db 37 LAALMALLIVATVGNALVLAFAVDSSLRQNNFFLNLAISDFLVGAFCIPLYVPVL 96  
Qy 78 F-NWNFGSGICMFWLITDYLLCTASVYVNLISYDRYQSVNAVSYRAQHTGIMKIYAQM 136  
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQOQDTRAVRKM 156  
Qy 137 VAVWILAFVNGPMLASDSWK-----NSTNTKDCPEGFVTEWYILITITMLLEFLLPVIS 191  
Db 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTFPLS 213

Qy 192 VAYFNVOIY-----WSLWKRRALSRCPSH 215  
Db 214 VTFNLSIYLNIOQRRLRLDCAEAGPEPPPEAQPSPPPPCGCMGCKQKHGSEAMPLH 273  
Qy 216 -----AGSTTSSASGHLHRAAGVACRTSNPGLKESAAASRHSESPRRKSSILVSLRT 267  
Db 274 RYGVGEAAVGAEGATELGGGGGSAASPTSSG-----SSSRGTERPR----- 318  
Qy 268 HNMSSITAFKVGFWRSSESALRQ-----EYAEALLRGRKLARSLLAISAFIACW 318  
Db 319 -----SLRKGSKPSASSASLEKRMKMWVSQFTQRFRLSRDRKVAKSLAVISIFGLCW 371  
Qy 319 APYCLFTIVLSTYRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKILCVT 378  
Db 372 APYLLMIIRAACHGCHVP-DYWTYETSWLLWANSVNPVLYPLCHHSFRRAFTKLCPQ 430  
Qy 379 K 379  
Db 431 K 431

## RESULT 14

US-09-165-543-5  
; Sequence 5, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-165-543-5

Query Match 35.0%; Score 716.5; DB 2; Length 445;  
Best Local Similarity 40.2%; Pred. No. 2.8e-51;  
Matches 165; Conservative 54; Mismatches 128; Indels 63; Gaps 10;

Qy 18 LAFIMSSFAFIMVGNNAVILAFVVDNRNLRHSRYFFLNLAISDFLVGLISIPLYIPHL 77  
Db 37 LAALMALLIVATVGNALVLAFAVDSSLRQNNFFLNLAISDFLVGAFCIPLYVPVL 96  
Qy 78 F-NWNFGSGICMFWLITDYLLCTASVYVNLISYDRYQSVNAVSYRAQHTGIMKIYAQM 136

Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSVRAQQGDTTRAVRKM 156  
QY 137 VAYWILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLEFLLPVIS 191  
Db 157 ALVWVLAFLYGGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213  
QY 192 VAYFNVQIYWSLWKRRAL-----SRCPSHAGFSTTSSSASGH-----LH 230  
Db 214 VTFNLSIYLNIQRRTRLRDGGREAGPEPPDAQPPSPPPSCWGCWPKHGGEAMPLH 273  
QY 231 RAGVACRTSNPGLK-----ESAAASHSESPPRKSILVSLRTHM 269  
Db 274 RYGVG--EAGPGVEAGEAALGGSGGGAASPTSSSGSSSRGTERPR-----SLKRG 324  
QY 270 NSSITAFKVGSGFWRSESAALRQREYAEALLRGRKLARSLAILLSAFAICWAPYCLFTIVLS 329  
Db 325 KPSASSASLEKRMKMWVSQSIQR--FRLSRDKKVAKSLAIIVSIFGLCWAPYTLMLIIRA 382  
QY 330 TYPRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKILCVTK 379  
Db 383 ACHGRCLP-DYWTETSFLLWANSVNPVLYPLCHYSFRRAFTKLLCPQK 431

## RESULT 15

US-09-891-053-25  
; Sequence 25, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891,053  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JP99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-891-053-25

Query Match 35.0%; Score 716.5; DB 2; Length 445;  
Best Local Similarity 40.2%; Pred. No. 2.8e-51;  
Matches 165; Conservative 54; Mismatches 128; Indels 63; Gaps 10;

QY 18 LAFLMSSGFALMGVNAVILAFVVDNRNLRHSNYFFLNLAISDFLVGLISIPLYIPHL 77  
Db 37 LAALMALLIVATVLGNALVMAFVADSSLRQNNFFLNLAISDFLVGAFCIPLYVPVL 96  
QY 78 F-NNPFGSGICMFWLITDYLCTASVNVNVLISYDRVQSVNAVSVYRAQHTGIMKIVAQM 136  
Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSVRAQQGDTTRAVRKM 156  
QY 137 VAYWILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLEFLLPVIS 191  
Db 157 ALVWVLAFLYGGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213  
QY 192 VAYFNVQIYWSLWKRRAL-----SRCPSHAGFSTTSSSASGH-----LH 230  
Db 214 VTFNLSIYLNIQRRTRLRDGGREAGPEPPDAQPPSPPPSCWGCWPKHGGEAMPLH 273

QY 231 RAGVACRTSNPGLK-----ESAAASHSESPPRKSILVSLRTHM 269  
Db 274 RYGVG--EAGPGVEAGEAALGGSGGGAASPTSSSGSSSRGTERPR-----SLKRG 324  
QY 270 NSSITAFKVGSGFWRSESAALRQREYAEALLRGRKLARSLAILLSAFAICWAPYCLFTIVLS 329  
Db 325 KPSASSASLEKRMKMWVSQSIQR--FRLSRDKKVAKSLAIIVSIFGLCWAPYTLMLIIRA 382  
QY 330 TYPRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKILCVTK 379  
Db 383 ACHGRCLP-DYWTETSFLLWANSVNPVLYPLCHYSFRRAFTKLLCPQK 431

Search completed: May 24, 2006, 13:35:39  
Job time : 30 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 24, 2006, 13:35:10 ; Search time 85 Seconds  
(without alignments)  
2130.788 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWALSONQSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main.\*  
1: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2048	100.0	391	5	US-10-626-445-8
2	2048	100.0	391	5	US-10-626-126-8
3	2048	100.0	391	5	US-10-626-398-8
4	1735	84.7	391	5	US-10-626-445-9
5	1735	84.7	391	5	US-10-626-126-9
6	1735	84.7	391	5	US-10-626-398-9
7	1370.5	66.9	390	3	US-09-812-216-2
8	1370.5	66.9	390	3	US-09-910-411-2
9	1370.5	66.9	390	3	US-09-875-076-14
10	1370.5	66.9	390	3	US-09-876-252-14
11	1370.5	66.9	390	3	US-09-852-165-2
12	1370.5	66.9	390	3	US-09-891-138A-6
13	1370.5	66.9	390	4	US-10-052-193-2
14	1370.5	66.9	390	4	US-10-225-567A-629
15	1370.5	66.9	390	4	US-10-272-983-14
16	1370.5	66.9	390	4	US-10-354-769-2
17	1370.5	66.9	390	4	US-10-393-807-14
18	1370.5	66.9	390	4	US-10-417-820A-14
19	1370.5	66.9	390	4	US-10-349-253A-2
20	1370.5	66.9	390	4	US-10-696-673-2
21	1370.5	66.9	390	4	US-10-723-555-14
22	1370.5	66.9	390	4	US-10-782-596-14
23	1370.5	66.9	390	4	US-10-737-619-2
24	1370.5	66.9	390	5	US-10-626-445-2
25	1370.5	66.9	390	5	US-10-684-206-20
26	1370.5	66.9	390	5	US-10-616-088-2
27	1370.5	66.9	390	5	US-10-626-126-2

28	1370.5	66.9	390	5	US-10-626-398-2	Sequence 2, Appli
29	1370.5	66.9	390	5	US-10-756-149-4702	Sequence 4702, Ap
30	1370.5	66.9	390	5	US-10-723-955-14	Sequence 14, Appli
31	1370.5	66.9	390	5	US-10-488-421-8	Sequence 8, Appli
32	1366.5	66.7	390	4	US-10-290-078-27	Sequence 27, Appli
33	1366.5	66.7	390	5	US-10-488-421-6	Sequence 6, Appli
34	1237	60.4	389	5	US-10-626-445-10	Sequence 10, Appli
35	1237	60.4	389	5	US-10-626-126-10	Sequence 10, Appli
36	1237	60.4	389	5	US-10-626-398-10	Sequence 10, Appli
37	1198	58.5	357	5	US-10-488-421-4	Sequence 4, Appli
38	1074.5	52.5	336	5	US-10-488-421-2	Sequence 2, Appli
39	729.5	35.6	415	5	US-10-495-679A-8	Sequence 8, Appli
40	722.5	35.3	445	3	US-09-350-206-2	Sequence 2, Appli
41	722.5	35.3	445	3	US-09-349-755-2	Sequence 2, Appli
42	722.5	35.3	445	3	US-09-166-334-2	Sequence 2, Appli
43	722.5	35.3	445	4	US-10-282-958-2	Sequence 2, Appli
44	722.5	35.3	445	4	US-10-225-567A-549	Sequence 549, App
45	722.5	35.3	445	4	US-10-453-106-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-10-626-445-8  
; Sequence 8, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-626-445-8

Query Match 100.0%; Score 2048; DB 5; Length 391;  
Best Local Similarity 100.0%; Pred. No. 6.8e-180;  
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSESNTGILPPAAQVPLAFILMSFAFIMVGNNAVILAFVVDRLNLRHRSNYFFLNLAIS	60
Db	1	MSESNTGILPPAAQVPLAFILMSFAFIMVGNNAVILAFVVDRLNLRHRSNYFFLNLAIS	60
Qy	61	DFLVGLISILYIYPHVLFNNFGSGICMFWLITDYLCTASVNVILISDYRYSVNAV	120
Db	61	DFLVGLISILYIYPHVLFNNFGSGICMFWLITDYLCTASVNVILISDYRYSVNAV	120
Qy	121	SYRAQHTGIMKIYVAQMVAVMILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILTIT	180
Db	121	SYRAQHTGIMKIYVAQMVAVMILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILTIT	180
Qy	181	MLLEFLLPVTSVAYFNVQIYVSWLKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN	240
Db	181	MLLEFLLPVTSVAYFNVQIYVSWLKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN	240
Qy	241	PGLKESAAHSHSPRKSILYSLRTHMNSSITAFKVGFWRSSEALRQREYAEILRG	300
Db	241	PGLKESAAHSHSPRKSILYSLRTHMNSSITAFKVGFWRSSEALRQREYAEILRG	300
Qy	301	RKLARSAILLSAFAICWAPYCLFTIIVLSTYPRTERPKSVWYSTAFWLOWNSFNPNFLY	360
Db	301	RKLARSAILLSAFAICWAPYCLFTIIVLSTYPRTERPKSVWYSTAFWLOWNSFNPNFLY	360

QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391  
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

## RESULT 2

US-10-626-126-8  
; Sequence 8, Application US/10626126  
; Publication No. US20050074770A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0033  
; CURRENT APPLICATION NUMBER: US/10/626,126  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-626-126-8

Query Match 100.0%; Score 2048; DB 5; Length 391;  
Best Local Similarity 100.0%; Pred. No. 6.8e-180;  
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNLRHRSNYFFLNLAIS 60  
Db 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNLRHRSNYFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFLLITDYLLCTASVNVNIVLISYDRYQSVNAV 120  
Db 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFLLITDYLLCTASVNVNIVLISYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIIVAQMVAVMILAFVNGPMLASDSWKNSITAFKVGFWKSESAAALQREYAEALLRG 180  
Db 121 SYRAQHTGIMKIIVAQMVAVMILAFVNGPMLASDSWKNSITAFKVGFWKSESAAALQREYAEALLRG 180  
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240  
Db 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240  
QY 241 PGLKESAAASHSPRRKSSILVSLRTHMNSSITAFKVGFWKSESAAALQREYAEALLRG 300  
Db 241 PGLKESAAASHSPRRKSSILVSLRTHMNSSITAFKVGFWKSESAAALQREYAEALLRG 300  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFLY 360  
Db 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFLY 360  
QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391  
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

## RESULT 3

US-10-626-398-8  
; Sequence 8, Application US/10626398  
; Publication No. US20050074841A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0034  
; CURRENT APPLICATION NUMBER: US/10/626,398  
; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-626-398-8

Query Match 100.0%; Score 2048; DB 5; Length 391;  
Best Local Similarity 100.0%; Pred. No. 6.8e-180;  
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNLRHRSNYFFLNLAIS 60  
Db 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNLRHRSNYFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFLLITDYLLCTASVNVNIVLISYDRYQSVNAV 120  
Db 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFLLITDYLLCTASVNVNIVLISYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIIVAQMVAVMILAFVNGPMLASDSWKNSITAFKVGFWKSESAAALQREYAEALLRG 180  
Db 121 SYRAQHTGIMKIIVAQMVAVMILAFVNGPMLASDSWKNSITAFKVGFWKSESAAALQREYAEALLRG 180  
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240  
Db 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240  
QY 241 PGLKESAAASHSPRRKSSILVSLRTHMNSSITAFKVGFWKSESAAALQREYAEALLRG 300  
Db 241 PGLKESAAASHSPRRKSSILVSLRTHMNSSITAFKVGFWKSESAAALQREYAEALLRG 300  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFLY 360  
Db 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFLY 360  
QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391  
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

## RESULT 4

US-10-626-445-9  
; Sequence 9, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-10-626-445-9

Query Match 84.7%; Score 1735; DB 5; Length 391;  
Best Local Similarity 84.7%; Pred. No. 4.7e-151;  
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNLRHRSNYFFLNLAIS 60

Db 1 MSESNGTDVPLPLTAQVPLAFVLSLAFVADRNLRHNSYFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120  
Db 61 DFFVGVISIPLYIPHTLFNNWPGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120  
Qy 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180  
Db 121 RYRAQHTGILKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180  
Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPHAGFSTTSSASGHLHRAGVACRTSN 240  
Db 181 AFLEFLLPVSLVYFVSQIYWSLWKRSLSRCPHAGFIATSSRGTHSRRTGLACRTSL 240  
Qy 241 PGLKESAASHSSPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILLRG 300  
Db 241 PGLKEPAASHSSPRKSSLLVSLRTHMSGSIIFKVGSCFSESPVLHQREHVELLRG 300  
Qy 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWFNFSVNPFLY 360  
Db 301 RKLARSLAVLSAFACWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWFNLSINPFLY 360  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSONOSVSS 391  
Db 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391

## RESULT 5

US-10-626-126-9  
; Sequence 9, Application US/10626126  
; Publication No. US20050074770A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0033  
; CURRENT APPLICATION NUMBER: US/10/626,126  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-10-626-126-9

Query Match 84.7%; Score 1735; DB 5; Length 391;  
Best Local Similarity 84.7%; Pred. No. 4.7e-151;  
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;  
Qy 1 MSESNGTGILPPAAQVPLAFVLSLAFVADRNLRHNSYFFLNLAIS 60  
Db 1 MSESNGTDVPLPLTAQVPLAFVLSLAFVADRNLRHNSYFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120  
Db 61 DFFVGVISIPLYIPHTLFNNWPGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120  
Qy 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180  
Db 121 RYRAQHTGILKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180  
Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPHAGFSTTSSASGHLHRAGVACRTSN 240  
Db 181 AFLEFLLPVSLVYFVSQIYWSLWKRSLSRCPHAGFIATSSRGTHSRRTGLACRTSL 240  
Qy 241 PGLKESAASHSSPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILLRG 300  
Db 241 PGLKEPAASHSSPRKSSLLVSLRTHMSGSIIFKVGSCFSESAALRQREYAEILLRG 300

Db 241 PGLKEPAASHSSPRKSSLLVSLRTHMSGSIIFKVGSCFSESPVLHQREHVELLRG 300  
Qy 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWFNFSVNPFLY 360  
Db 301 RKLARSLAVLSAFACWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWFNLSINPFLY 360  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSONOSVSS 391  
Db 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391

## RESULT 6

US-10-626-398-9  
; Sequence 9, Application US/10626398  
; Publication No. US20050074841A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0034  
; CURRENT APPLICATION NUMBER: US/10/626,398  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-10-626-398-9

Query Match 84.7%; Score 1735; DB 5; Length 391;  
Best Local Similarity 84.7%; Pred. No. 4.7e-151;  
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;  
Qy 1 MSESNGTGILPPAAQVPLAFVLSLAFVADRNLRHNSYFFLNLAIS 60  
Db 1 MSESNGTDVPLPLTAQVPLAFVLSLAFVADRNLRHNSYFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120  
Db 61 DFFVGVISIPLYIPHTLFNNWPGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120  
Qy 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180  
Db 121 RYRAQHTGILKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180  
Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPHAGFSTTSSASGHLHRAGVACRTSN 240  
Db 181 AFLEFLLPVSLVYFVSQIYWSLWKRSLSRCPHAGFIATSSRGTHSRRTGLACRTSL 240  
Qy 241 PGLKESAASHSSPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILLRG 300  
Db 241 PGLKEPAASHSSPRKSSLLVSLRTHMSGSIIFKVGSCFSESPVLHQREHVELLRG 300  
Qy 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWFNFSVNPFLY 360  
Db 301 RKLARSLAVLSAFACWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWFNLSINPFLY 360  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSONOSVSS 391  
Db 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391

## RESULT 7

US-09-812-216-2  
; Sequence 2, Application US/09812216  
; Publication No. US20020098539A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu

```
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match      66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY      1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MPTDNTINLSLSTRVTLAFMNSLVAFAIMLGNALVILAFVVDKRLRHSRYFFLNLAIS 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLITDYLLCTASVNIIVLISVDRYQSVNAV 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 DFFVGVISIPLYIPIHVLFNWFGSGICMFWLITDYLLCTASVNIIVLISVDRYQSVNAV 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      121 SYRAQHTGIMKIIVAOVAVMVLAFVNGPMILASDSWKNSTNTKDCPPGFVTEWYILIT 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121 SYRTQHTGVILKIVTLVAVVWVLAFLVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      181 MLEFLLPVISVAYFNVOIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      179 SFLEFVIPVILVAYFNWNIYWSLWKRDHLSCQSHPLGTAVSSNICHSFRGLSSRRSL 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      241 PGLKESAASHRSERPRKSSILVSLRTHMNSSITAFKVGSWFSESAALRQREYAEILLRG 300
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      239 SASTEVPASPHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVLHQREHVELLRA 298
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      301 RKLARSLAILLSAFATCWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      299 RRLAKSLAILLGVFVAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPFY 358
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      359 PLCHKRFQKAFKIFCICKQKPLPSQHSRVS 390
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

Query Match      66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY      1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MPTDNTINLSLSTRVTLAFMNSLVAFAIMLGNALVILAFVVDKRLRHSRYFFLNLAIS 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLITDYLLCTASVNIIVLISVDRYQSVNAV 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 DFFVGVISIPLYIPIHVLFNWFGSGICMFWLITDYLLCTASVNIIVLISVDRYQSVNAV 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      121 SYRAQHTGIMKIIVAOVAVMVLAFVNGPMILASDSWKNSTNTKDCPPGFVTEWYILIT 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121 SYRTQHTGVILKIVTLVAVVWVLAFLVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      181 MLEFLLPVISVAYFNVOIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      179 SFLEFVIPVILVAYFNWNIYWSLWKRDHLSCQSHPLGTAVSSNICHSFRGLSSRRSL 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      241 PGLKESAASHRSERPRKSSILVSLRTHMNSSITAFKVGSWFSESAALRQREYAEILLRG 300
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      239 SASTEVPASPHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVLHQREHVELLRA 298
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      301 RKLARSLAILLSAFATCWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      299 RRLAKSLAILLGVFVAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPFY 358
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      359 PLCHKRFQKAFKIFCICKQKPLPSQHSRVS 390
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-875-076-14
; Sequence 14, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liao, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match 66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSSNSGILPPAAQVPLAFMLSFAPAIMVGNNAVILAFVVDNLRHRSYFFLNLAIS 60
DB 1 MPDNTNSTINLSLSTRTVLTAFFMSLVAFAIMLGNALVILAFVVDNLRHRSYFFLNLAIS 60
QY 61 DFLVGLTISILYIPHLVFNWFGGICWFWLITDYLCTASVNVILISYDRYQSVSNV 120
DB 61 DFFVGVLISILYIPHLTFFWDGKEICVFWLITDYLCTASVNVILISYDRYQSVSNV 120
QY 121 SYRAQHTGIMKIVAQVAVMILAFVNGPMILASDWKNTNTKDCBPGFVTEWYILIT 180
DB 121 SYRQHTGVILKIVTMVAVVLAFLVNGPMILVSESNKDEGS--ECBPGFVTEWYILIT 178
QY 181 MLLEFLLPVLSVAYFNVQIYWSLWKRALSRCPSHAGFSTTSSASGHLHRAGVACTSN 240
DB 179 SFLEFVLPVILVAYFNNIYWSLWKRDHLRQCQSHGLTAVSSNICGHSFGRLLSSRSL 238
QY 241 PGLKESAASHSESPPRKSSTLVSLRTHMNSSITAFKVGFSFWRSESAAALRQREYAEILLRG 300
DB 239 SASTEVPAFSHSEQRKRSLSMFSSRTYMSNTTASKMGFSQSDSVALLQREHVELLRA 298
QY 301 RKLARSLAILLSAFACWAPCYCLFTIVLSTYPTERTPKSVMYSTAFWLQFNFSVNPFLY 360
DB 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVMYRIAFWLQFNFSVNPFLY 358
QY 361 PLCHRRFOKAFKILCVTKWPAISO--NQSVSS 391
DB 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 10
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.

; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match          66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNRNLRHRSYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSYFFLNLAIS 60

QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHTLFEMDFGKEICVFWLTITDYLCTASVNVILISYDRYLSVNAV 120

QY 121 SYRAQHTGIMKIIVAQMVAVMILAFLVNPGMILASDSWKNSTNTKDCBPFGVTEWYILIT 180
DB 121 SYRTQHTGVLIKIVTLMVAVVWLAFLVNPGMILVSESWKDEGS--ECEPGPFSEWYILAIT 178

QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVIPVLIVAYFNNIYWSLWKRDHLSCQSHPGLTAVSSNICGHSFRGLSSRRSL 238

QY 241 PGLKESAASHSSPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALQREYAEILRG 300
DB 239 SASTEVPAFPHSERQRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298

QY 301 RKLARSLAILLSAFACWAPCYCLFTIVLSTYPRTERPKSVWYSIAFWLOWFNSFVNPLY 360
DB 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLOWFNSFVNPLY 358

QY 361 PLCHRRFQKAFMKILCVTKWPALSO-NQSVSS 391
DB 359 PLCHKRFQKAFKLFCIKKQPLFSQHSRSVSS 390

RESULT 11
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1 G Protein-Coupled Receptors
; FILE REFERENCE: 00231regus
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2

Query Match          66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNRNLRHRSYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSYFFLNLAIS 60

QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHTLFEMDFGKEICVFWLTITDYLCTASVNVILISYDRYLSVNAV 120

QY 121 SYRAQHTGIMKIIVAQMVAVMILAFLVNPGMILASDSWKNSTNTKDCBPFGVTEWYILIT 180
DB 121 SYRTQHTGVLIKIVTLMVAVVWLAFLVNPGMILVSESWKDEGS--ECEPGPFSEWYILAIT 178
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DB 121 SYRTQHTGVLIKIVTLMVAVVWLAFLVNPGMILVSESWKDEGS--ECEPGPFSEWYILAIT 178
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVIPVLIVAYFNNIYWSLWKRDHLSCQSHPGLTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAASHSSPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALQREYAEILRG 300
DB 239 SASTEVPAFPHSERQRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFACWAPCYCLFTIVLSTYPRTERPKSVWYSIAFWLOWFNSFVNPLY 360
DB 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLOWFNSFVNPLY 358
QY 361 PLCHRRFQKAFMKILCVTKWPALSO-NQSVSS 391
DB 359 PLCHKRFQKAFKLFCIKKQPLFSQHSRSVSS 390

RESULT 12
US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1el Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match          66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNRNLRHRSYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSYFFLNLAIS 60

QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHTLFEMDFGKEICVFWLTITDYLCTASVNVILISYDRYLSVNAV 120

QY 121 SYRAQHTGIMKIIVAQMVAVMILAFLVNPGMILASDSWKNSTNTKDCBPFGVTEWYILIT 180
DB 121 SYRTQHTGVLIKIVTLMVAVVWLAFLVNPGMILVSESWKDEGS--ECEPGPFSEWYILAIT 178

QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVIPVLIVAYFNNIYWSLWKRDHLSCQSHPGLTAVSSNICGHSFRGLSSRRSL 238

QY 241 PGLKESAASHSSPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALQREYAEILRG 300
DB 239 SASTEVPAFPHSERQRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298

QY 301 RKLARSLAILLSAFACWAPCYCLFTIVLSTYPRTERPKSVWYSIAFWLOWFNSFVNPLY 360
DB 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLOWFNSFVNPLY 358
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QY 361 PLCHRRFQKAFKILCVTKWPAALSO-NQSVSS 391  
Db 359 PLCHRRFQKAFKILCVTKWPAALSO-NQSVSS 390

RESULT 13

US-10-052-193-2

; Sequence 2, Application US/10052193

; Publication No. US20020132755A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer, Inc.

; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS

; FILE REFERENCE: PC10963A

; CURRENT APPLICATION NUMBER: US/10/052,193

; CURRENT FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: 0101223.6

; PRIOR FILING DATE: 2001-01-17

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 2

; LENGTH: 390

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-052-193-2

Query Match 66.9%; Score 1370.5; DB 4; Length 390;

Best Local Similarity 68.1%; Pred. No. 1.8e-117;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSPFAIMVGNVILAFVVDNLRHRSYFFLNLAIS 60

Db 1 MPDNTSTINLSLSTRVTLAFMFLVAFIMLGNALVILAFVVDNLRHRSYFFLNLAIS 60

QY 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120

Db 61 DFFVGVISIPLYIPHLFNDGKEICVFWLITDYLCTASVNVILISYDRYQSVNAV 120

QY 121 SYRAQHTGIMKIVAQVAVMVLAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180

Db 121 SYRTQHTGVLKIVTLMAVAVVLAFLVNGPMLVSESWKDEGS--ECBPGGFSEWYILAIT 178

QY 181 MLLEFLLPVLSVAYFNVQIYWSLWKRRLSRCPSHAGFSTSSASGHLHRAGVACTSN 240

Db 179 SFLEFVIPVTLVAYFNNIYWSLWKRDLHSLRCQSHPLGTAVSSNICGHSFRGLSSRRSL 238

QY 241 PGLKESAARSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWRSESAALRQREYAEILRG 300

Db 239 SASTEPASPHERQRRKSSIMFSSTRTKMNSNTIASKMGFSQSDSVLHQREHVELLRA 298

QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYISIAFWLQWFSVFNPLLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIRIAFWLQWFSVFNPLLY 358

QY 361 PLCHRRFQKAFKILCVTKWPAALSO-NQSVSS 391

Db 359 PLCHRRFQKAFKILCVTKWPAALSO-NQSVSS 390

RESULT 14

US-10-225-567A-629

; Sequence 629, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 629

; LENGTH: 390

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-629

Query Match 66.9%; Score 1370.5; DB 4; Length 390;

Best Local Similarity 68.1%; Pred. No. 1.8e-117;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSPFAIMVGNVILAFVVDNLRHRSYFFLNLAIS 60

Db 1 MPDNTSTINLSLSTRVTLAFMFLVAFIMLGNALVILAFVVDNLRHRSYFFLNLAIS 60

QY 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120

Db 61 DFFVGVISIPLYIPHLFNDGKEICVFWLITDYLCTASVNVILISYDRYQSVNAV 120

QY 121 SYRAQHTGIMKIVAQVAVMVLAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180

Db 121 SYRTQHTGVLKIVTLMAVAVVLAFLVNGPMLVSESWKDEGS--ECBPGGFSEWYILAIT 178

QY 181 MLLEFLLPVLSVAYFNVQIYWSLWKRRLSRCPSHAGFSTSSASGHLHRAGVACTSN 240

Db 179 SFLEFVIPVTLVAYFNNIYWSLWKRDLHSLRCQSHPLGTAVSSNICGHSFRGLSSRRSL 238

QY 241 PGLKESAARSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWRSESAALRQREYAEILRG 300

Db 239 SASTEPASPHERQRRKSSIMFSSTRTKMNSNTIASKMGFSQSDSVLHQREHVELLRA 298

QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYISIAFWLQWFSVFNPLLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIRIAFWLQWFSVFNPLLY 358

QY 361 PLCHRRFQKAFKILCVTKWPAALSO-NQSVSS 391

Db 359 PLCHRRFQKAFKILCVTKWPAALSO-NQSVSS 390

RESULT 15

US-10-272-983-14

; Sequence 14, Application US/10272983

; Publication No. US20030148450A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Ruoping

; APPLICANT: Dang, Huong T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

; FILE REFERENCE: AREN0050

; CURRENT APPLICATION NUMBER: US/10/272,983

; CURRENT FILING DATE: 2002-10-17

; PRIOR APPLICATION NUMBER: US/09/417,044

; PRIOR FILING DATE: 1999-10-12

; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16

; PRIOR APPLICATION NUMBER: 60/121,851

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/136,436

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,437

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,439

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,567

; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 390

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-272-983-14

Query Match 66.9%; Score 1370.5; DB 4; Length 390;  
Best Local Similarity 68.1%; Pred. No. 1.8e-117;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY	1	MSESNSTGILPPAAQVPLAFMSFAPAFMVGNAVILAFVVDNLRHRSNYPFLNLAIS	60
Db	1	MPDTNSTINLSLSTRVTLAFPMFLVAFALMGNALVILAFVVDNLRHRSSYFFLNLAIS	60
QY	61	DFLVGLISIPLYIPHYLVFNWFGSGICMEFWLIITDYLLCTASVYNIIVLISYDRYQSVNAV	120
Db	61	DFPVGVISIPLYIPHYLVFNWFGSGICMEFWLIITDYLLCTASVYNIIVLISYDRYLSVNAV	120
QY	121	SYRAQHTGIMKIVAQVAVMILAFVNGPMILASDSWKNSNTNTKDCPPGVTEWYILITIT	180
Db	121	SYRTQHTGVLIKIVLMVAVMILAFVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT	178
QY	181	MLLEFLLPVISVAYFNQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN	240
Db	179	SFLFVPVILVAYFNQIYWSLWKRRDLHLSRCQSHPLGTAVSSNICGHSFGRLSRRSL	238
QY	241	PGLKESGAASHSESPPRRKSSILVSLRTHMNSSITAFKVGSGFMRSESAALRQREYAEILRG	300
Db	239	SASTEVPASPHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVLHQREHVELLRA	298
QY	301	RKLARSLAILLSAPACWAPCYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPFY	360
Db	299	RRLAKSLAILLGFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLY	358
QY	361	PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS	391
Db	359	PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS	390

Search completed: May 24, 2006, 13:37:10  
Job time : 86 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 24, 2006, 13:35:45 ; Search time 10 Seconds  
(without alignments)  
435.470 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New\*

- 1: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1366.5	66.7	390	7	US-11-242-505A-27
2	295.5	14.4	357	7	US-11-302-678-38
3	295.5	14.4	359	6	US-10-511-937-2990
4	292.5	14.3	440	7	US-11-302-678-41
5	283	13.8	269	7	US-11-305-477-3
6	267	13.0	465	7	US-11-255-699-4
7	236.5	11.5	403	7	US-11-242-505A-18
8	214.5	10.5	364	7	US-11-255-699-1
9	206.5	10.1	362	7	US-11-312-958-24
10	206.5	10.1	366	7	US-11-255-699-2
11	206	10.1	423	7	US-11-312-958-12
12	204	10.0	380	7	US-11-302-678-20
13	203	9.9	368	6	US-10-511-937-2505
14	203	9.9	368	6	US-10-511-937-2931
15	203	9.9	368	7	US-11-302-678-59
16	200.5	9.8	384	7	US-11-304-129-36
17	200.5	9.8	384	7	US-11-312-958-6
18	199.5	9.7	378	6	US-10-511-937-2404
19	197.5	9.6	412	7	US-11-242-505A-15
20	196.5	9.6	381	7	US-11-304-129-49
21	196.5	9.6	393	7	US-11-304-129-1
22	196.5	9.6	393	7	US-11-312-958-8
23	195.5	9.5	389	7	US-11-302-678-35
24	192	9.4	421	7	US-11-304-129-47
25	189	9.2	360	7	US-11-257-851A-75

26	187	9.1	393	7	US-11-304-129-40	Sequence 40, Appl
27	187	9.1	393	7	US-11-304-129-48	Sequence 48, Appl
28	178.5	8.7	352	6	US-10-505-328-745	Sequence 745, App
29	178.5	8.7	352	6	US-10-511-937-2935	Sequence 2935, Ap
30	178.5	8.7	352	6	US-10-511-937-2935	Sequence 2935, Ap
31	178.5	8.7	352	6	US-10-511-937-3010	Sequence 3010, Ap
32	175	8.5	350	6	US-10-511-937-2609	Sequence 2609, Ap
33	173	8.4	352	6	US-10-511-937-2412	Sequence 2412, Ap
34	165.5	8.1	370	7	US-11-305-477-1	Sequence 1, Appl
35	164	8.0	297	7	US-11-257-851A-73	Sequence 73, Appl
36	159.5	7.8	360	7	US-11-242-111-19	Sequence 19, Appl
37	158	7.7	360	7	US-11-242-505A-3	Sequence 3, Appl
38	157.5	7.7	352	7	US-11-242-505A-6	Sequence 6, Appl
39	156.5	7.6	332	7	US-11-257-851A-77	Sequence 77, Appl
40	156	7.6	325	7	US-11-312-958-40	Sequence 40, Appl
41	156	7.6	325	7	US-11-257-851A-79	Sequence 79, Appl
42	155	7.6	373	7	US-11-312-958-10	Sequence 10, Appl
43	151	7.4	424	7	US-11-242-505A-33	Sequence 33, Appl
44	151	7.4	424	7	US-11-255-699-3	Sequence 3, Appl
45	137	6.7	351	6	US-10-511-937-2540	Sequence 2540, Ap

ALIGNMENTS

RESULT 1

US-11-242-505A-27  
; Sequence 27, Application US/11242505A  
; Publication No. US20060099656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: Hematological Disorders for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; FILE REFERENCE: WPI2001-288P1RCP1OWNIM  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-242-505A-27

Query Match 66.7%; Score 1366.5; DB 7; Length 390;  
Best Local Similarity 67.9%; Pred. No. 4.2e-111;  
Matches 266; Conservative 40; Mismatches 83; Indels 3; Gaps 2;

QY	1	MSENSTGILPPAAQVPLAFMSSFAIMVGNVILAFVVDENLRHSNYFFLNLAIS	60
Db	1	MPDTNSTINLSLSTRVTLFAFMGLNALVILAFVVDKLRHSYFFLNLAIS	60
QY	61	DFLVGLTISPLYPHVLFFNNFGSGICMFWLITDYLCTASVYVNLISYDRYQSVSNV	120
Db	61	DFVGVVTSIPLYPHTLFEWDFGKEICVFWLITDYLCTASVYVNLISYDRYLSVSNV	120
QY	121	SYRAQHTGIMKIYQAVVAVMILAFVNGPMILASDSWKNSTNTKDCBPGFVTEWILTIT	180
Db	121	SYRQHTGVGLKIVTLVMVAVVLAFLVNGPMILVSESWKDEGS--ECPGPFSEWYLAIT	178
QY	181	MLLEFLLPVTSVAYFNVQIYWSLWKRLSRCSHAGFTSTSSASGHLHRAAGVACRTSN	240
Db	179	SFLEFVPIVLVAYFNNMNIYWSLWKRLSRCSHGLTVSSNICGHSFGRLSRRSL	238

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QY 241 PGLKESAAHRSSEPRKSSILVSLRTHMNSSITAPKVGFWSESAALRQREVAELRG 300
Db 239 SASTEPASTSHERRRRKSSSRRTKGMNSTIASXGSGFSQSDSVALRQREHVELLRA 298
QY 301 RKLARSILAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLOWFNSFVNPFY 360
Db 299 RRLAKSLAILLGVAVCWAPYSFTIVLSFYSSATGPKSVWYRIAPFWLOWFNSFVNPLY 358
QY 361 PLCHRPQKAFWKILCVTKWPALSO-NQSVSS 391
Db 359 PLCHKRQKAFKIFCIIKQPLSPQHSRVSS 390

RESULT 2
US-11-302-678-38
; Sequence 38, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Venkateswarlu, Karicheti
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1RM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-38

Query Match 14.4%; Score 295.5; DB 7; Length 357;
Best Local Similarity 24.5%; Pred. No. 1.5e-18;
Matches 89; Conservative 72; Mismatches 132; Indels 71; Gaps 15;

QY 18 LAFILM--SSEFAIMVGNNAVILAFVVDRLNLRH--SNFYFNLAIISDFLVGLISIPYIPH 75
Db 47 LGFLVAATFAWLLV-----LATILRTRTHRVPHNLVMSVSDVLVAALVMPLSLVH 100
QY 76 VLF--NNNFGSGICMFWLITDYLLCTASVYVNLISYDRYQSVSNVSVYRAQHTGIMKIV 133
Db 101 ELSGRRLGRRLCOLWIACDVLCCITASINWNTAIALDRYWSITRHEMYTLR---TRKCV 157
QY 134 AQ-MWAV-WTILAFVNGPMILASDWSKNSTNKKDC-----EPGFVTEWYIITITMLLEFL 187
Db 158 SNVMIALTWALSAVISLAPLLFGWGETYSEGSECVSRSPSYA-----VFSTVGAFYL 211
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QY 188 PVISVAFVNVQIYVSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSNPGLKESA 247
Db 212 PLCVLF-----VWKYKKA-----KFRVGSRTKNSVSPISE 244
QY 248 ASHSSSPRRKSSILVSLRTHMNSSITAFKVGFWSESAALRQREVAELRGKRLARSL 307
Db 245 AVEVKDSAKQPMVF---TVRHATVTFQEGDTWREQ-----KEQRAALMV 287
QY 308 AILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLOWFNSFVNPLYPLCHRRF 367
Db 288 GILIGVFLVCWIPFEL-TELISPLCSDIP-AIWKSIFLWLGYSNSFNFLLIYTAFNKY 345
QY 368 QKAF 371
Db 346 NSAF 349

RESULT 3
US-10-511-937-2990
; Sequence 2990, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2990
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2990

Query Match 14.4%; Score 295.5; DB 6; Length 359;
Best Local Similarity 24.1%; Pred. No. 1.5e-18;
Matches 90; Conservative 64; Mismatches 126; Indels 93; Gaps 12;

QY 13 AAQVPLAFLMSSFAFIMVGNNAVILAFVVDRLNLRHNSFYFNLAIISDFLVGLISIPL- 71
Db 16 ACKTITTVLAVLILITVAGNVVCLAVGLNRLRLNLTNCFIVSLAITDLLGLLPLPFS 75
QY 72 YIPHLFNNWFGSGICMFWLITDYLLCTASVYVNLISYDRYQSVSNVSVYRAQHTGIMK 131
Db 76 AIYQLSCKSGFGVFCNCIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPVLVTPV-R 134
QY 132 IVAQMVAVTILAFVNGPMILASDWSKNSTN-----TKDCEPGFVTEWYIITITMLLEFL 186
Db 135 VALSLVLIVISITLSFLSLIHGLWNSERNETSKGNHHTTSCKVKQ-VNEVYGL-VDGLVTYF 192
QY 187 LP--VISVAFNVQIYVSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSNPGLK 244
Db 193 LPLLIMCITYRI-----FKVARDQA----- 213
QY 245 ESAASHRSSEPRKSSILVSLRTHMNSSITAFKVGFWSESAALRQREVAELRGKLA 304
Db 214 -----KRINHI-----SSWK-----AATIREHKA 233
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Query Match	14.3%	Score 292.5;	DB 7;	Length 440;
Best Local Similarity	24.4%;	Pred. No. 3.5e-18;		
Matches	95;	Conservative 74;	Mismatches 153;	Indels 67; Gaps 13;
QY	4	SNST---	GILPPAAQVFLAFMSFATAIMV---	GNAAVILAFVVDRLRHRSNYFFLNL 57
DB	9	ANSTPAWGAGPPS	APGSGWVAALCVVIALTAAANSLLI	ALICTQPAINTSNFFLVSL 68
QY	58	AISDFLVGLISIP	LYIPHVLP-NNPFGSGICMFMLITD	YLLCTTASVNVILISYDRQSV 116
DB	69	FTSDLMVGLVVP	PMALNALLYGRVTLARGICLLTAF	DMCCSASILNLCILISIDRYLLI 128
QY	117	SNASVYRAOHTG	IMKIVQAQVAVVILAFLVNG-PMILAS	DSWKNSTNTKCEPG---FVT 172
DB	129	LSPLRYKLRWTP	-LRALALVLGAWSLAALASFLLLL--	GWELGHARPPVPQCRLLA 184
QY	173	EWILTTMTLLE	FLLPVISAIVNFVQIYWSLWKERALS	RCPDSHAGFTTSSASGLHRA 232
DB	185	SLFPVLVASGLT	FTFLPSPGACICTFYCRILLAA-RKQAV	QVQVSLTFTGM---ASQASETIQ-- 238
QY	233	GVACRTSNPGL	KESAARSHGESPRKGSILVSLRTHMNS	ITATFKVSGFWFRSESAALRQR 292

RESULT 6  
US-11-255-699-4  
; Sequence 4, Application US/11255699  
; Publication No. US20060105393A1  
; GENERAL INFORMATION:  
; APPLICANT: APPEL, CHRISTIAN  
; APPLICANT: ENDERLE, THILLO  
; APPLICANT: ZOPFMAN, SANNAH  
; APPLICANT: PENSKI, MIRELE  
; APPLICANT: JENSENSEN



Db 157 KLAS--AAAWVLSLMSLPLLVFADVQBGTCNASWPPEVGLWGAVFIITAVLGFAPL 214  
Qy 189 -VISVAFNVQIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSNGLKESA 247  
Db 215 LVICLCVLLIIV-----KVRA-----AGVRVGC 237  
Qy 248 ASRHSRPRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRQREYAEALLRGRKLARS 307  
Db 238 VRRSE-----  
Qy 308 AILLSAFAICWAPYCLFTIVLSTYRTERPKSV-WYSIAFWLWNFNSFVNPFLYPLCHRR 366  
Db 251 LVVLVVFAGCWLPFTVNVINLAVALPOEPASAGLFPFVILSVANSANCANPVLYGELSDN 310  
Qy 367 FQKAFWKILCVTK 379  
Db 311 FROSQFVKVLCIRK 323

RESULT 9  
US-11-312-958-24  
; Sequence 24, Application US/11312958  
; Publication No. US20060100152A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Rosenfeld, Julie Beth  
; APPLICANT: Silos-Santiago, Inmaculada  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,  
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,  
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,  
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55034, 16314, 1613, 1675, 9569 OR  
; TITLE OF INVENTION: 13424 MOLECULES  
; FILE REFERENCE: MPI02-027P1RNOXNM  
; CURRENT APPLICATION NUMBER: US/11/312,958  
; CURRENT FILING DATE: 2005-12-20  
; PRIOR APPLICATION NUMBER: US/10/369,022  
; PRIOR FILING DATE: 2003-02-19  
; PRIOR APPLICATION NUMBER: US 60/360,495  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/370,121  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 60/373,010  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/373,908  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/377,717  
; PRIOR FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: US 60/379,949  
; PRIOR FILING DATE: 2002-05-13  
; PRIOR APPLICATION NUMBER: US 60/382,409  
; PRIOR FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/385,280  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US 60/386,879  
; PRIOR FILING DATE: 2002-06-06  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-312-958-24

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Best Local Similarity 19.5%; Pred. No. 7.5e-11;  
Matches 74; Conservative 71; Mismatches 129; Indels 105; Gaps 9;

Qy 11 PPAQVPLAFLMSSFAFAIMVGNVAVITLAFVVDRLNRHSNYFFLNLAISDFLVGLISIP 70  
Db 36 PPWAPALSAVLIVTTAVDVGVNLLVILSVLRNKRKNAGNLFVLVSALADLVVAFYPYP 95

Qy 71 LYIPHLVFN-WNFGSGICMEFWLITDYLLCTASVYVNIIVLISDRYQSVSNAYS-----YRAQ 125  
Db 96 LIIVAIFYDGHGALGEHCKASAFVWGLSVGVSNITAIINRYCYICHSMAYHRIYRW 155  
Qy 126 HTGIMKIVAQVAVMILAFVNGPMILASDKMKNSTNTKCEPGFVTEWYILTTIT- 180  
Db 156 HTPL-----HICLIWLLTWALLBNFF-----VGSLEYDPRISCTFIOTASTQYTA 202  
Qy 181 --MLLEFLLPVISVAYFNVOIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRT 238  
Db 203 AVVVIHEFLPIAVVSFCYLRIMVILQAR-----RK 233  
Qy 239 SNPKESASARHSESPPRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRQREYAE 298  
Db 234 AKP-----ESRLCPKPSDLRSLTWF----- 254  
Qy 299 RGRKLARSALILSFAFAICWAPYCLFTIVLSTYRTERPK--SVWYSIAFWLWNFNSFVN 356  
Db 255 -----VVFVIFALCWAPLNCIGLAVAINQEMAPQIPEGLFVTSYLLAVFNSCLN 304

Qy 357 PFLYPLCHRRFQKAFWKIL 375  
Db 305 AIVYGLLNQNFREYKRIL 323

RESULT 10  
US-11-255-699-2  
; Sequence 2, Application US/11255699  
; Publication No. US20060105393A1  
; GENERAL INFORMATION:  
; APPLICANT: APPEL, CHRISTIAN  
; APPLICANT: ENDERLE, THILLO  
; APPLICANT: ZOFFMANN, SANNAH JENSEN  
; APPLICANT: PENSKI, MIREILLE  
; TITLE OF INVENTION: LIGAND-RECEPTOR TRACKING ASSAYS  
; FILE REFERENCE: 22817  
; CURRENT APPLICATION NUMBER: US/11/255,699  
; CURRENT FILING DATE: 2005-10-21  
; PRIOR APPLICATION NUMBER: EP 04105285.3  
; PRIOR FILING DATE: 2004-10-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-255-699-2

Query Match 10.1%; Score 206.5; DB 7; Length 366;  
Best Local Similarity 21.1%; Pred. No. 7.6e-11;  
Matches 82; Conservative 74; Mismatches 112; Indels 121; Gaps 18;

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Db 41 PLLAGVATCTVALFVVGCIAGNLLTMLVVSRELRITTNLYLSMAFSDLLI-FLCPLD 99  
Qy 72 -----YIPHLFNNWFGSGIC-MFWLITDYLLCT-ASVYVNIIVLISDRYQSVSNAYS 123  
Db 100 LVRLWQVRP-----WNFGDLLCKLFQVSE--SCTVATVLTITALSVERYFAICFPLRAK 152  
Qy 124 AQHT-GIMKIVAQVAVMILAFVNGPM-ILASDSWKNST---NTKCEP-GFVTEWYIL 177  
Db 153 VVVTGRVKLV--IFVIVAVAFCSAGIFVLVGVHEHNGTDPWDTNECRPTFAVRSGLL 210  
Qy 178 TITMLLE---FLLPVISVAYFNVOIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGV 234  
Db 211 TVWVWVSSIFFLPVFCLTVLYSLIGRKLWR----- 242  
Qy 235 ACRTSNPGLKESASARHSESPPRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRQREY 294  
Db 243 -----RRGDVV-----GASLRDQNH 258  
Qy 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYRTERPKSVWYS-----IAF 346









GenCore version 5.1.8  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 25, 2006, 13:51:33 ; Search time 7472 Seconds  
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Title: US-10-626-445-8

-Perfect score: 2048

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Ygapop 10.0 , Ygapext 0.5  
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Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
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6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2035	99.4	1538	6 AF358859	Mus muscu
2	1745	85.2	1593	6 AF358860	Rattus no
3	1682.5	82.2	1308	6 BC111862	Mus muscu

C	4	1434.5	70.0	199837	6	AC131672	Mus muscu
	5	1372.5	67.0	1173	5	AY008280	Homo sapi
	6	1370.5	66.9	1173	2	AX142850	Sequence
	7	1370.5	66.9	1173	2	BD015847	Novel pol
	8	1370.5	66.9	1173	2	CS173186	Sequence
	9	1370.5	66.9	1173	2	CS178018	Sequence
	10	1370.5	66.9	1173	2	AR391860	Sequence
	11	1370.5	66.9	1173	2	AX109119	Sequence
	12	1370.5	66.9	1173	2	AX139113	Sequence
	13	1370.5	66.9	1173	2	AX301763	Sequence
	14	1370.5	66.9	1173	5	AF307973	Homo sapi
	15	1370.5	66.9	1173	5	AF325356	Homo sapi
	16	1370.5	66.9	1173	5	AF329449	Homo sapi
	17	1370.5	66.9	1173	5	AY136745	Homo sapi
	18	1370.5	66.9	1173	5	HS298292	Homo sapi
	19	1370.5	66.9	1266	2	AX376577	Sequence
	20	1370.5	66.9	1300	2	AX301229	Sequence
	21	1370.5	66.9	1312	2	BD095598	Novel gua
	22	1370.5	66.9	1312	5	AB045370	Homo sapi
	23	1370.5	66.9	1316	5	BC069136	Homo sapi
	24	1370.5	66.9	1847	5	BC112348	Homo sapi
	25	1370.5	66.9	3689	2	AX549343	Sequence
	26	1366.5	66.7	1227	2	BD097512	Novel gua
	27	1366.5	66.7	1265	5	AB044934	Homo sapi
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	29	1357.5	66.3	1175	5	AB189711	Macaca fa
	30	1311.5	64.0	1291	14	AB053300	Sus scrof
	31	1238	60.4	1451	6	AF358858	Cavia por
C	32	1199	58.5	236694	12	AC118386	Rattus no
	33	1064	52.0	1950	2	CQ947118	Sequence
C	34	906	44.2	140555	5	AC007922	Homo sapi
C	35	906	44.2	166206	12	AC009668	Homo sapi
C	36	906	44.2	167296	12	AP002507	Homo sapi
C	37	906	44.2	169144	5	AC090244	Homo sapi
C	38	906	44.2	184938	12	AP002476	Homo sapi
	39	906	44.2	193779	12	AP001327	Homo sapi
	40	731.5	35.7	1311	2	DD165407	HISTAMINE
	41	724.5	35.4	1401	2	DD165404	HISTAMINE
	42	724.5	35.4	2685	2	CQ730452	Sequence
	43	724.5	35.4	2689	2	AR104201	Sequence
	44	724.5	35.4	2689	2	BD086285	G protein
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#### ALIGNMENTS

RESULT 1	AF358859	1538 bp	linear	ROD 02-SEP-2001
LOCUS	Mus musculus histamine H4 receptor mRNA, complete cds.			
DEFINITION	AF358859			
ACCESSION	AF358859.1			
VERSION	GI:15420534			
KEYWORDS	Mus musculus (house mouse)			
SOURCE	Mus musculus			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 1538)			
AUTHORS	Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.			
TITLE	Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 1538)			
AUTHORS	Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.			
TITLE	Direct Submission			
JOURNAL	Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA			
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	/mol_type="mRNA"			

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/db xref="taxon:10090"
61_1236
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STTSASGHLHRAVACSTPGLKESASRSPRRKSSILVSLRTHMNSISIAF
KVGSPWRSSEALRQREYAEALLRKLARSLAILLSAFAICWAPYCLFTIVLSTYPT
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ORIGIN

Alignment Scores:
Pred. No.: 7,43e-202 Length: 1538
Score: 2035.00 Matches: 390
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.4% Indels: 0
DB: 6 Gaps: 0

US-10-626-445-8 (1-391) x AF358859 (1-1538)

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QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
DB 121 TTAATGTCCTCATTTGCTTTGCTATTAATGCTAGGCAATGCTGGTCATCTTAGCCCTT 180
QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 181 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCTT 240
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
DB 241 GACTTCTCTGGTGGTTTGATTTCCATTCCTGTACATCCCTCACGCTGTTGTTAACTGG 300
QY 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100
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QY 121 SerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMetValAlaValTyr 140
DB 421 TCTTATAGGCTCAACACACCTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTG 480
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160
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QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
DB 541 ACGACACAAAGAGCTGTAGCCCTGGCTTTGTACACAGTGGTACATCTCCACCATTAACA 600
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DB 601 ATGCTCTTGGAAATTCCTGCTCTCTGTCATCTCTGCTGCTTATTTCAATGATACAGATTAC 660
QY 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 661 TGGAGCTGTGGAGCGTAGGCTCTCAGTAGGTCCTCAGTAGGTCCTCAGCAGTCTGATTTCCACT 720
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QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
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QY 341 TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
DB 1081 TGGTACAGCATTCCTTCTGGCTGCAATGCTTCAATTCGTTTGAATCCCTTCTCTGTAC 1140
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyr 380
DB 1141 CTTTGTGTACAGGCTTTCAGAGGCTTTCGAGAGTACTTTTGTGTGACAAAGCAA 1200
QY 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
DB 1201 CCAGCGCTGTCCACAGAACCAAGTCAGTATCTTCT 1233

RESULT 2
AF358860 1593 bp mRNA linear ROD 02-SEP-2001
LOCUS Rattus norvegicus histamine H4 receptor mRNA, complete cds.
DEFINITION AF358860
ACCESSION AF358860.1 GI:15420536
VERSION
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 1593)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation
Unpublished
2 (bases 1 to 1593)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
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CDS
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IATSSRCTGHSRRRTGLACRTSLPGLKEPAAHLHSESPRGKSSLLVSLRTHMSGSIAP  
KVGSFCSRSESPVLHOREHVELLRKRLARSALVLSAFYCAICWAPYCFITVLSTYRRG  
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## ORIGIN

Alignment Scores:  
Pred. No.: 1,5e-171 Length: 1593  
Score: 1745.00 Matches: 332  
Percent Similarity: 89.3% Conservatives: 17  
Best Local Similarity: 84.9% Mismatches: 42  
Query Match: 85.2% Indels: 0  
DB: 6 Gaps: 0

US-10-626-445-8 (1-391) x AF358860 (1-1593)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaGlnValProLeuAlaPhe 20  
Db 36 ATGTCGGAGTCTAACGGCACTGACGCTCTGCACTGCTCAAGTCCCTCGCATTT 95  
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
Db 96 TTAATGTCCCTGCTGCTTTTGTCTATACGATAGCAATGCTGTGCTCATTTTAGCCTTT 155  
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 156 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTT 215  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
Db 216 GACTTCTTCGTGGGTGCATCTCCATCTCTGTACATCCCTCACGCTGTTAACTGG 275  
Qy 81 AspPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrLeuLeuCysThrAla 100  
Db 276 AATTTTGGAAAGTGAATCTGCATGTTTGGCTATTACTGACTATCTTTGTGCACAGCA 335  
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 336 TCCGCTCTACAGTATGTGCTCAATAGCTACCATGATGATACCATGCTGTTCAAGCGCTGTG 395  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140  
Db 396 CGTTATAGACACACACACATGGCATCTCGAATTTGTTCTCAATGTTGGCTGTTGG 455  
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160  
Db 456 ATACTGCTTTCTTGGTCAATGGCCCAATGATCTGCTGCTCGGATCTTGGAGAACAGC 515  
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180  
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Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 576 GCATCTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTCTATTTCAGTGTACAGATTAC 635  
Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
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Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
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Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260  
Db 756 CTGTGATTAAGGAACACAGCGCATCCCTTCATTCAGAAAGTCCACGAGGAAGAGCAGT 815  
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280  
Db 816 CTCCTGTGTCTTTAAGACTCATCATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 875  
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300

Db 876 TTCTGCCGATCAGAAAGCCAGTCCTTCCACGAGAGACGCTGGAGCTTCTCAGAGGC 935  
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 936 AGGAAGCTAGCAGCTCGTAGCTTCTCTCTGAGTCTTTTGGCATTTTGTGGCTCCG 995  
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
Db 996 TATTGCTGTTTCAAAATGTTCTTTCAACTTATCCGAGAGGGAGCGCCCAATTCGATT 1055  
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360  
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Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391  
Db 1176 CCAGCCTTTCCAGACCCAGCTCAGTATCTTCT 1208  
RESULT 3  
LOCUS BC111862 1308 bp mRNA linear ROD 16-JAN-2006  
DEFINITION Mus musculus histamine H4 receptor, mRNA (cDNA clone MGC:130500  
IMAGE:40046148), complete cds.  
ACCESSION BC111862  
VERSION BC111862.1 GI:84993254  
KEYWORDS MGC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 1308)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshyuki, S.,  
Carroll, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Vallal, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shavchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smal, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Mammalian Gene Collection Program Team  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1308)  
NITH MGC Project  
Direct Submission  
Submitted (13-JAN-2006) National Institutes of Health, Mammalian  
Gene Collection (MGC) Bethesda, MD 20892-2590, USA  
NITH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: mgc-help desk  
Email: gcapbs-x@mail.nih.gov  
Tissue Procurement: Baylor Human Genome Sequencing Center  
cDNA Library Preparation: Baylor Human Genome Sequencing Center  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nih.gov/>

Contact: nisc.mcconhgr@nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 Maduro, O.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
 Tourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAM Plate; 15 Row; C Column: 19.

## FEATURES

Location/Qualifiers

1..1308

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="MGC:130500 IMAGE:40046148"

/tissue\_type="PCR rescued clones"

/clone\_lib="NIH\_MGC\_285"

/notes="Vector: PCR-Blunt II-TOPO with reversed insert;

Clone identification sequence tag: GTGGTTA"

## gene

1..1308

/gene="Hrh4"

/notes="synonyms: H4, H4R, BG26, HH4R, AXOR35, GPRV53,

GPCR105"

/db\_xref="GeneID:225192"

/db\_xref="MGI:2429635"

283..1071

/gene="Hrh4"

/codon\_start=1

/product="Hrh4 protein"

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/db\_xref="GI:84933255"

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/db\_xref="MGI:2429635"

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 AGVACRTSNPLKESASRHSSEPRKRSILVLRTHMNSITAFKVGSPWRSSEAL  
 ROEYAEALLRGLKRLASLAILLSAFALICWAPYCLFTIVLSTYPRTERPKSVMYSIAPW  
 LQWFNSFVNFFPLCHRRRQKFKILCVTKQPALSQNSQSVSS"

## ORIGIN

## Alignment Scores:

Pred. No.:	3,71e-165	Length:	1308
Score:	1682.50	Matches:	334
Percent Similarity:	85.2%	Conservative:	0
Best Local Similarity:	85.2%	Mismatches:	2
Query Match:	82.2%	Indels:	56
DB:	6	Gaps:	1

US-10-626-445-8 (1-391) x BC111862 (1-1308)

Qy	1	MetSerGlnSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe	20
Db	60	ATGTGCGAGTCTAACAGTACTGGCATCTGCCACAGCTGCTCAGGTCCTTGGCAATTT	119
Qy	21	LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe	40
Db	120	TTAATGTCCTCAATTTGGCTTTGCTATATATGGTAGCAATGCTGGGTCACTTAGCCCTTT	179
Qy	41	ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	180	GTGTGTGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCT	239
Qy	61	AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr	80
Db	240	GACTTCCTC-----	248
Qy	81	AsnPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrLeuLeuCysThrAla	100

Db	248	-----	248
Qy	101	SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAla-Va	120
Db	249	-----	254
Qy	120	lSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTr	140
Db	255	GTCTTATAGGCTCAACACACATCGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTG	314
Qy	140	pIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSe	160
Db	315	GATACTGGCTTTCTTGGTAAATGCCGATGATTTCTGGCTTCAGATTCTTTGGGAAGACAG	374
Qy	160	rThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTrpIleLeuThrIleTh	180
Db	375	CACGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCCACATTAC	434
Qy	180	rMetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTy	200
Db	435	AATGCTCTTGGAAATTCCTGCTTCTCTCATCTCTGTGGCTTATTTCATGTACAGATTAA	494
Qy	200	rTrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerTh	220
Db	495	CTGGAGCCTGTGGAAGCGTAGGCTCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCAC	554
Qy	220	rThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAs	240
Db	555	TACCTCTTCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAA	614
Qy	240	nProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSe	260
Db	615	TCTTGGATTGAAGGAATCAGTGCATCTCTCTCAGAAAGTCTCTCGAAGAAAGACAG	674
Qy	260	rIleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySe	280
Db	675	CATCTGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCCTTCAAAGTGGGTTTC	734
Qy	280	rPheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGl	300
Db	735	CTTCTGGCGATCGGAAGTGCAGCGCTTCCCAAAGGAGTACGACAGCTTCTCAGAGG	794
Qy	300	YArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPr	320
Db	795	CAGGAAGCTAGCCAGGTCACCTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCC	854
Qy	320	oTyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVa	340
Db	855	ATACTGTCTGTTCAACAATTGCTCTTCACTTACCCAGAACCGCCCAAAATCGGT	914
Qy	340	lTyrTrpSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTy	360
Db	915	GTGGTACAGCATTTGCCCTTCTGGCTGCAATGGTTCAATTCGTTTGTATCCCTTCTGTA	974
Qy	360	rProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTr	380
Db	975	CCCTTTGTGTACAGGGCTTTCAGAAGGCTTTCGAAGATACTTTGTGTGACAAAGCA	1034
Qy	380	pProAlaLeuSerGlnAsnGlnSerValSerSer	391
Db	1035	ACCAGCGCTGTACAGAACCAAGTCAGTATCTTCT	1068

## RESULT 4

AC131672/c

LOCUS

DEFINITION

AC131672

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC131672 199837 bp DNA linear ROD 11-FEB-2004  
 Mus musculus chromosome UNK clone RP23-314021, complete sequence.

AC131672

AC131672.3 GI:42517281

HTG.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 199837)

Wilson, R.K.

The sequence of Mus musculus clone

Unpublished

2. (bases 1 to 199837)

McPherson, J.D. and Waterston, R.H.

Direct Submission

Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

3. (bases 1 to 199837)

Wilson, R.K.

Direct Submission

Submitted (06-NOV-2003) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

4. (bases 1 to 199837)

Wilson, R.K.

Direct Submission

Submitted (11-FEB-2004) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

On Feb 11, 2004 this sequence version replaced gi:38194370.

## COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>

Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)

----- Project Information -----

Center project name: M.BA0314021

----- Location/Qualifiers -----

1. 199837

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

/chromosome="UNK"

/clone="RP23-314021"

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.82e-136 Length: 199837  
 Score: 1434.50 Matches: 296  
 Percent Similarity: 78.6% Conservative: 13  
 Best Local Similarity: 75.3% Mismatches: 33  
 Query Match: 70.0% Indels: 51  
 DB: 6 Gaps: 8

US-10-626-445-8 (1-391) x AC131672 (1-199837)

Qy	12	ProAlaAlaGlnValPro-----	-----LeuAlaPheLeuMetSer	23
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Qy	24	SerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPheValValAsp	43	
Db	93399	GCCTTCTATTAGATA-----	GTGTCATGCTTGTCTACAGTGT	93358
Qy	44	ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAppPheLeu	63	
Db	93357	TCAAACTT---CACCTGATGGTGTATGTTGTCTTGACAGTTATTGAGAAAGCATGT	93301	
Qy	64	ValGlyLeu-----IleSerIleProLeuTyrIleProHisValLeuPheAsnTyrAsn	81	
Db	93300	GCCACATCAGTCAGTAGTAGCTTGCATATCCC-----	TGAAC	93256
Qy	82	PheGlySerGlyIleCysMetPheTrpLeu-----IleThrAspTyrLeuLeuCys	98	
Db	93255	-----ARGTGTTTTTCATTAACACCATTAAGTTAGTGTCTGTTCTTG-----	93214	
Qy	99	ThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn	118	
Db	93214	-----	93214	

Qy	119	AlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAla	138
Db	93213	TAGGTGCTTTATAGGGCTCAACACATGGCATTCATGAAGATTGTTGCTCAATGGTGGCT	93154
Qy	139	ValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLys	158
Db	93153	GTTTGGATACCTGGCTTTCTTGGTAAATGGCCCGATGATTCCTGGCTTCAGATCTCTGGAG	93094
Qy	159	AsnSerThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThr	178
Db	93093	AACAGCAGCAACACAAAGGACTGTGACCTGGCTTTGTTACAGAGTGTGTACATCCTCACC	93034
Qy	179	IleThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGln	198
Db	93033	ATTACAATGCTTTGGAAATTCCTGCTTCATCTCTGTGGCTTATTTCAATGTACAG	92974
Qy	199	IleTyrTrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPhe	218
Db	92973	ATTACTGGAGCCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATCTGGATTC	92914
Qy	219	SerThrThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThr	238
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Qy	239	SerAsnProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLys	258
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Qy	259	SerSerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysVal	278
Db	92793	AGCAGCATCCTGGTGTCTTAAAGACTCACATGAACAGCAGTATCACCTCCCTTCAAAAGTG	92734
Qy	279	GlySerPheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeu	298
Db	92733	GGTTCTTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAGGGAGTAGCAGAGAGCTTCTC	92674
Qy	299	ArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrp	318
Db	92673	AGAGGCAGGAAGTAGCCAGTCACTGGCCATCTTCTGAGCGCTTTTGGCATTTGCTTGG	92614
Qy	319	AlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLys	338
Db	92613	GCTCCATACCTGCTGTGTTCACAAATTTGCTTCACTTACCTCCAGAACGGAACGCCCAAA	92554
Qy	339	SerValTrpTyrSerIleAlaPheTrpPheAsnSerPheValAsnProPhe	358
Db	92553	TCGGTGTGTACAGCATTTGCTTCTGCTGCAATGGTTCATTCGTTTGTATATCCCTTT	92494
Qy	359	LeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThr	378
Db	92493	CTGTACCTTTGTGTACAGCGCTTTCAGAAGGCTTCTGGAAGATACATTGTGTGACA	92434
Qy	379	LysTrpProAlaLeuSerGlnAsnGlnSerValSerSer	391
Db	92433	AAGCAACACGCGCTGTACAGAACCCAGTCAGTATCTTCT	92395

## RESULT 5

LOCUS	AY008280	1173 bp	mRNA	linear	PRI 15-MAR-2004
DEFINITION	Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.				
ACCESSION	AY008280				
VERSION	AY008280.1	GI:15822540			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1. (bases 1 to 1173)				
AUTHORS	Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K., Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and O'Dowd, B.F.				





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ORIGIN
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Alignment Scores:
Pred. No.: 1.19e-132 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2 Gaps: 2

US-10-626-445-8 (1-391) x AR142850 (1-1173)

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Db 1 ATGCCAGATACATAATAGCACAAATTTATCACTAAGCACTCGTGTACTTAGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATGCTAGAAATGCTTTGGTCAATTTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
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Db 181 GACTTCTTTGTGGTGTGATCTCCATCCCTTTGTATCATCCCTCACACGCTGTTCGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTyrIleThrAspTyrIleLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTAGCTACATCTGTTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTGTCCTCATCAGCATATGATCATCTGTCAGTCTCAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTCTTACTCTGATGGTGGCGGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 GTCTGGCCCTCTTAGTGAATGGCCCAATGATTTCTTAGTTTCAGAGCTTTGGAAGGAGAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTTGCCATCACA 534
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RESULT 7
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LOCUS Novel polypeptide. 1173 bp DNA linear PAT 27-AUG-2002
DEFINITION BD015847
ACCESSION BD015847
VERSION BD015847.1 GI:22556984
KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Peter,B. and Olaylee,M.A.
TITLE Novel polypeptide
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;
PRIZER INC
COMMENT OS Homo sapiens (human)
PN JP 2001211889-A/1
PD 07-AUG-2001
PF 27-OCT-2000 JP 2000329359
PR 29-OCT-1999 GB 9925641:4, 20-APR-2000 GB 0009973:9 PI
BEAT PETER, MARK ANTONY OLAYLEE
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P1/04,
PC A61P11/00,
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Pred. No.: 1.19e-132 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2 Gaps: 2

US-10-626-445-8 (1-391) x BD015847 (1-1173)
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CS173186 LOCUS CS173186 1173 bp DNA linear PAT 05-OCT-2005
DEFINITION Sequence 13 from Patent EP1580271.
ACCESSION CS173186
VERSION CS173186.1 GI:77153219
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Chen,R.
Human Orphan G Protein-Coupled Receptors
Patent: EP 1580271-A 13 SEP-2005;
Arena Pharmaceuticals, Inc. (US)
Hominidae; Homo.
REFERENCE 1
AUTHORS Chen,R.
TITLE Human Orphan G Protein-Coupled Receptors
JOURNAL Patent: EP 1580271-A 13 SEP-2005;
Arena Pharmaceuticals, Inc. (US)
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Location/Qualifiers
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Alignment Scores: 1.19e-132 Length: 1173
Pred. No.: 1370.50 Matches: 267
Score: 1370.50 Conservative: 40
Percent Similarity: 78.3% Mismatches: 82
Best Local Similarity: 68.1% Indels: 3
Query Match: 66.9% Gaps: 2
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LOCUS Sequence 13 from Patent EP1584683.
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ACCESSION CS178018.1 GI:77733617
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
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AUTHORS Chen, R.
TITLE Human orphan g protein-coupled receptors
JOURNAL Patent: EP 1584683-A 13 12-OCT-2005;
ARENA Pharmaceuticals, Inc. (US)
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Pred. No.: 1.19e-132 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2 Gaps: 2

US-10-626-445-8 (1-391) x CS178018 (1-1173)
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Score:              1370.50        Matches:    267
Percent Similarity: 78.3%          Conservative: 40
Best Local Similarity: 68.1%       Mismatches:  82
Query Match:        66.9%          Indels:     3
DB:                 2              Gaps:        2

US-10-626-445-8 (1-391) x AX109119 (1-1173)

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Db 715 TCTGCATCGACAGAAAGTCTCTGATCTCTTCAATTCAGAGAGACAGAGAGAAAGAGTAGT 774
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
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Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
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Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTTCTTAGGGGTTTGTCTTGTCTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 955 TATTCTCTGTTTCAAAATTTGCTTTTCAATTTTATTTTCTCAGCAACAGGTCCTTAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGAATTGCAATTTGGCTTTCAGTGGTTCAAATTCCTTTGTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTACAAAGCGCTTTCAAAGGCTTTCTTGAAATATATTTGTATATAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
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RESULT 12
AX139113          1173 bp      DNA      linear      PAT 30-MAY-2001
LOCUS             Sequence 1 from Patent EP1096009.
ACCESSION         AX139113
VERSION           AX139113.1 GI:14274791
KEYWORDS           Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM           Homo sapiens
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                   Homnidae; Homo.
REFERENCE
AUTHORS           Peter, B. and O'Reilly, M.A.
TITLE             G-protein coupled receptor-like polypeptide
JOURNAL           Patent: Ep 1096009-A 1 02-MAY-2001;
                   Pfizer Limited (GB) ; PFIZER INC. (US)
FEATURES           Location/Qualifiers
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                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

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Score:              1370.50        Matches:    267
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Best Local Similarity: 68.1%       Mismatches:  82
Query Match:        66.9%          Indels:     3
DB:                 2              Gaps:        2

US-10-626-445-8 (1-391) x AX139113 (1-1173)

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Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180
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Db 715 TCTGCATCGACAGAGTTCCTGCTATCTTCAATTCAGAGACAGAGAGAGAGTAGT 774
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Qy 281 PheTrpArgSerGluSerAlaLeuLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
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Db 1075 CCATTGTGTACACAGCGCTTTCAAAAGGCTTCTTGTAAAATATTTTGTATAAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTCTACCATCACAAACAGTCGCTGATCTCTCT 1170
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## RESULT 13

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AX301763 LOCUS AX301763 1173 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 1 from Patent WO0185786.
ACCESSION AX301763
VERSION AX301763.1 GI:17382844
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H.
TITLE Human histamine h 4? receptor
JOURNAL Patent: WO 0185786-A 1 15-NOV-2001;
American Home Products Corporation (US)
FEATURES
source 1. 1173
Location/Qualifiers
/organism="Homo sapiens"
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## ORIGIN

## Alignment Scores:

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Pred. No.: 1.19e-132 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2 Gaps: 2
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US-10-626-445-8 (1-391) x AX301763 (1-1173)

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Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTCTTAGTACCTTTTGTATAATCTAGGAATGCTTTGGTCAATTTAGCTTT 120
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Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTTGGGTGTGATCTCCATCTTTGTACATCTCTCACGCTGTTGCAATGG 240
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Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
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Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
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Db 535 TCATTTCTGGAATTCGTGATCCCATCTAGTCTTATTTTCAACATCAATATTTAT 594
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Qy      341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db      1015 TGGTATAGAAATGCAATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTTGTAT 1074
Qy      361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1075 CCATTGTGTCAACAGCGCTTTCAAAAGGCTTTCTTGAAATAATTTTGTATATAAAAGCAA 1134
Qy      381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
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Search completed: May 25, 2006, 15:57:13  
Job time : 7533 secs



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 24, 2006, 23:49:27 ; Search time 1232 Seconds  
(without alignments)  
3319.175 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
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Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues  
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : N Geneseq 8: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1370.5	66.9	1170	9	AAD55126	Aad55126 Human H4
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6	1370.5	66.9	1173	3	AAD01124	Aad01124 Human GPC
7	1370.5	66.9	1173	4	AAF83203	Aaf83203 Human GPC
8	1370.5	66.9	1173	5	AAH24007	Aah24007 Human G p
9	1370.5	66.9	1173	6	ABZ80663	Abz80663 Human his
10	1370.5	66.9	1173	6	ABQ78739	Abq78739 Nucleotid
11	1370.5	66.9	1173	6	AAI70980	Aai70980 Human his
12	1370.5	66.9	1173	6	AAI67750	Aai67750 Human his
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ALIGNMENTS

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ID AAI70981 standard; CDNA; 1176 BP.  
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AC AAI70981;  
XX  
DT 18-MAR-2002 (first entry)  
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DB Mouse histamine H4 receptor cDNA.  
XX  
KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy; ss.  
XX  
OS Mus musculus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;

XX WPI: 2002-114339/15.  
 DR P-PSDB; AAM50565.  
 XX  
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 XX Claim 4; Fig 5A; 92pp; English.  
 PS  
 XX The present sequence is that of a cDNA clone encoding a murine histamine  
 CC receptor of the H4 subtype. The cDNA was isolated from a mouse spleen  
 CC cDNA library. It shows 72.8% homology to the human H4 receptor coding  
 CC region. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
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 Score: 2035.00 Matches: 390  
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 Db 1021 TGGTACAGCATTCGCTTCTGGCTGCAATGTTCAATTCGTTGTTAATCCCTTCTCTGTAC 1080  
 Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyr 380  
 Db 1081 CCTTTGTGTACAGCGCTTTCAGAGAGCTTTCTGGNAGATACTTTGTGTGACAAAGCAA 1140  
 Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391  
 Db 1141 CCAGCGCTGTCCACAGAACCAAGTCAGTATCTTCT 1173

RESULT 2  
 ADO30257  
 ID ADO30257 standard; cDNA; 1538 BP.  
 XX  
 AC ADO30257;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Mouse GPCR HRH4 polynucleotide, SEQ ID NO:1360.  
 XX  
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; immune disorder; bone disorder;  
 KW muscular disorder; blood disorder; nutritive disorder; cancer;  
 KW joint disorder; metabolic disorder; lung disorder; breast disorder;  
 KW kidney disorder; liver disorder; prostate disorder; testis disorder;  
 KW ovary disorder; uterus disorder; pancreas disorder; spleen disorder;  
 KW skin disorder; stomach disorder; antiparkinsonian; antimanic;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
 KW cytosatic; antinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;  
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
 KW murine; gene; ss.  
 XX  
 OS Mus musculus.

XX WO2004040000-A2.  
 XX PN  
 XX PD  
 XX PF 13-MAY-2004.  
 XX PF 09-SEP-2003; 2003WO-US028226.  
 XX PR 09-SEP-2002; 2002US-0409303P.  
 XX PR 09-APR-2003; 2003US-0461329P.  
 XX PA (PRIM-) PRIMAL INC.  
 XX PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 XX PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
 XX DR P-PSDB; ADO29497.  
 XX DR WPI; 2004-390329/36.  
 XX PT Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX PS Claim 151; SEQ ID NO 1360; 542pp; English.  
 XX CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridise to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
 CC nucleic acid of the invention. Note: The full sequence data for this  
 CC patent did not form part of the printed specification; those sequences  
 CC not shown were obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

## XX SQ Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3,07e-171 Length: 1538  
 Score: 2035.00 Matches: 390  
 Percent Similarity: 99.7% Conservative: 0  
 Best Local Similarity: 99.7% Mismatches: 1  
 Query Match: 99.4% Indels: 0  
 DB: 12 Gaps: 0

US-10-626-445-8 (1-391) x ADO30257 (1-1538)

Qy 1 MetSerGluSerAsnSerThrGlyIleuProAlaGlnValProLeuAlaPhe 20  
 Db 61 ATGTGGAGTCTAACAGTACTGGCATCTTGGCCACGCTGCTCAGGTCCCTTGGCAATT 120

Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleuAlaPhe 40  
 Db 121 TTAATGCTTTCATTTGGCTTTATTAATGCTAGGCAATGCTGGTCAATCTTAGCCCTTT 180  
 Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 Db 181 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT 240  
 Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80  
 Db 241 GACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCACGCTGTGTTAACTGG 300  
 Qy 81 AsnPheGlySerGlyIleCysMetPheTrpIleuIleThrAspTyrLeuLeuCysThrAla 100  
 Db 301 AATTTTGGAGTGGAACTGTCATGTTTGGGTCATTACTGACTATCTTTTGTGCACCGCA 360  
 Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 Db 361 TCTGCTACAAATATTTGCTCTCATTTAGCTACGATACCACTCAGTTTCAAATGCTGTG 420  
 Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMetValAlaValTrp 140  
 Db 421 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 480  
 Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIysAsnSer 160  
 Db 481 ATACTGGCTTTCTTGGTAAATGGCCCGATGATCTGGCTTCAGATTTCTTGAAGAACAGC 540  
 Qy 161 ThrAsnThrIysAspCysGlyProGlyPheValThrGluTyrTrpTyrIleLeuThrIleThr 180  
 Db 541 ACGAACACAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCCACCATTTACA 600  
 Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
 Db 601 ATGCTCTTGGAAATTCCTGCTCTGCTCATCTCTGCTTATTTCAATGTACAGATTTC 660  
 Qy 201 TrpSerLeuTrpIysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
 Db 661 TGGAGCCTCTGGAAAGCGTAGGGCTCTCAGTAGTGTCCTAGCCATGCTGGAGTTCTCCA 720  
 Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
 Db 721 ACCTCTTCCAGTGTCTTCCAGACACTTTACACAGAGCTGGGTGGCTTCGACGACAAAGT 780  
 Qy 241 ProGlyLeuIysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260  
 Db 781 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGAGCAGC 840  
 Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280  
 Db 841 ATCTGTGTGCTCTTAAGGACTCACAATGAACAGCAGTAGTATCACTGCTTCAAAGTGGGTTCC 900  
 Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
 Db 901 TTTCTGGCGATCGGAAGAGTGAGGCTTCGCCAAAGGGAGTAGCGAGAGCTTCTCAGAGGC 960  
 Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 Db 961 AGNAGCTACCGAGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA 1020  
 Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
 Db 1021 TACTGTCTGTTCAAATTTGCTTCACTTACCTCCCAAGACGGAAACGCCCCCAATCGGTG 1080  
 Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
 Db 1081 TGGTACAGCATTCCTTCTGGCTGCAATGGTTCAAATTCGTTTGTATTCCTTCTGTGTAC 1140  
 Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpIysIleLeuCysValThrLysTrp 380  
 Db 1141 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTCTGGAAGATACCTTTGTGTGACAAAGCAA 1200  
 Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391

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Db      1201 CCAGCGCTGTGCACAGCAACGAGTCACTATCTCT 1233
RESULT 3
AAI70982
XX      1201 CCAGCGCTGTGCACAGCAACGAGTCACTATCTCT 1233
AC      AAI70982;
XX      18-MAR-2002 (first entry)
XX      Rat histamine H4 receptor cDNA.
DE      Histamine H4 receptor; rat; antiasthmatic; antiallergenic;
KW      antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW      diagnosis; gene therapy; ss.
XX      Rattus rattus.
XX      W0200192485-A1.
XX      06-DEC-2001.
XX      22-FEB-2001; 2001WO-US005914.
XX      31-MAY-2000; 2000US-0208260P.
XX      (ORTH ) ORTHO-MCNEIL PHARM INC.
XX      Lovenberg T, Liu C;
XX      WPI: 2002-114339/15.
XX      P-PSDB; AAM50566.
XX      New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT      the proteins, useful in gene therapy for treating diseases where it is
PT      beneficial to elevate mammalian histamine H4 receptor activity.
XX      Claim 4; Fig 5C; 92pp; English.
XX      The present sequence is that of a cDNA clone encoding a rat histamine
CC      receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA
CC      library. It shows 72.5% homology to the human H4 receptor coding region.
CC      The invention provides mammalian (human, mouse, rat and guinea pig)
CC      histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
CC      polypeptides (see AAM50564-67). The nucleic acids have been expressed in
CC      recombinant host cells that produce active recombinant protein. The
CC      pharmacology of known histamine ligands is demonstrated. Mammalian
CC      histamine H4 receptor may be used in gene therapy for the treatment of
CC      diseases where it is beneficial to elevate mammalian histamine H4
CC      receptor activity. Recombinant protein is useful for identifying
CC      modulators of the mammalian histamine H4 receptor. Such modulators may be
CC      useful for diagnosing, treating or preventing asthma, allergy,
CC      inflammation, cardiovascular and cerebrovascular disorders, non-insulin
CC      dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
CC      disorders of the neuroendocrine system, stress and spasticity
XX      Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1.47e-145      Length:      1176
Score:          1745.00      Matches:      332
Percent Similarity: 89.3%      Conservative: 17
Best Local Similarity: 84.9%      Mismatches: 42
Query Match:    85.2%      Indels:      0
DB:             6      Gaps:        0

US-10-626-445-8 (1-391) x AAI70982 (1-1176)
Qy      1 MetSerGluSerAsnSerThrGlyLeuLeuProAlaAlaGlnValProLeuAlaPhe 20
Db      1 ATGTCGGAGTCTAAACGGCACTGACGTCTTGCCACTGACTGCTCAAGTCCCTCGCATTT 60

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QY 381 ProAlaLeuSerGln---AenGlnSerValSerSer 391  
 DB 1135 CCTTACCATCACACACAGTCGGTACGATCTTCT 1170  
 RESULT 5  
 ID AAA46023 standard; cDNA; 1173 BP.  
 XX  
 AC AAA46023;  
 XX  
 DT 22-AUG-2000 (first entry)  
 XX Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.  
 DE Human G protein coupled receptor; GPCR; transmembrane receptor;  
 KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
 KW ss.  
 XX Homo sapiens.  
 OS  
 XX WO200022131-A2.  
 XX 20-APR-2000.  
 XX 13-OCT-1999; 99WO-US024065.  
 PF 13-OCT-1998; 98US-00170496.  
 PR 12-NOV-1998; 98US-0108029P.  
 PR 20-NOV-1998; 98US-0109213P.  
 PR 27-NOV-1998; 98US-0110060P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123944P.  
 PR 12-MAR-1999; 99US-0123945P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123948P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 12-MAR-1999; 99US-0123951P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 28-MAY-1999; 99US-0137567P.  
 PR 23-JUN-1999; 99US-0141448P.  
 PR 27-AUG-1999; 99US-0151114P.  
 PR 01-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX (AREN-) ARENA PHARM INC.  
 XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;  
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
 XX WPI; 2000-317986/27.  
 DR P-PSDB; AAB02831.  
 XX Non-endogenous, human G protein-coupled receptors for screening receptor,  
 PT inverse or partial agonists useful as therapeutic agents.  
 XX Example 1; Page 88-89; 187pp; English.  
 PS  
 XX

CC The present invention describes transmembrane receptors, preferably human  
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is  
 CC unknown (orphan GPCR receptors). More specifically the present invention  
 CC relates to non-endogenous, constitutively activated versions of a human  
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
 CC identification of candidate compounds as receptors agonists, inverse  
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3,49e-112 Length: 1173  
 Score: 1370.50 Matches: 267  
 Percent Similarity: 78.3% Conservative: 40  
 Best Local Similarity: 68.1% Mismatches: 82  
 Query Match: 66.9% Indels: 3  
 DB: Gaps: 2

US-10-626-445-8 (1-391) x AAA46023 (1-1173)

QY 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20  
 DB 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTAGCAATT 60  
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40  
 DB 61 TTTATGTCCTTAGTACTTTTGTATTAAGCTAGGAAATGCTTGGTCATTTTAGCTTTT 120  
 QY 41 ValValAspAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGGCATCTCT 180  
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
 DB 181 GACTTCTTTGTGGTGTGATCTCCATTCCTTTGTATACCTCCACACGCTGTTCGAATGG 240  
 QY 81 AsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCAGTACTGACTATCTGTATGTACAGCA 300  
 QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATAACATTGTCTCATCAGCTATGATCGATACCTGTCACTCTCAAAATGCTGTG 360  
 QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140  
 DB 361 TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTACTCTGATGGTGGCGGTTTG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160  
 DB 421 GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGICTTTCGAAGAGTAA 480  
 QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTrpIleLeuThrIleThr 180  
 DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAATGGTACATCTCTTGCATCACA 534  
 QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
 DB 535 TCATTCTTGGAAATTCGTGATGCCAGATCATCTTAGTCGCTTATTTCACATGAATATTAT 594  
 QY 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
 DB 595 TGGAGCCTGTGGAAAGCGTGATCATCTCAGTAGTGCCAAAGCCATCTCTGGAGTGTCT 654  
 QY 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
 DB 655 GTCTCTTCCAAACATCTGTGGACACTATTTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714  
 QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisGluSerProArgArgLysSerSer 260  
 DB 715 TCTGCATCGACAGAAGTTCTCTGCATCTCTTCTTCAATTCAGAGACAGAGAGAGATAGT 774



Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280  
Db 775 CTCATGTTTCTCCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTCC 834  
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAGGGAACATGTGAACCTGCTTAGAGCC 894  
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 895 AGGAGATTAGCCAAGTCACTGCCATTCTCTAGGGGTTTGTGCTTTGCTGGGCTCCA 954  
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
Db 955 TATTCTCTGTTCACAATGTCTTTCATTATTTATTTCTCAGCAACAGAGGTCCTAAATCAGTT 1014  
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTCCTTTTGCAATCTCTTTTGAT 1074  
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380  
Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGGCTTCTTGAAAATATTTGTATATAAAGCAA 1134  
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391  
Db 1135 CCTCTACCATCAACACAGTCGCTCAGTATCTTCT 1170  
RESULT 6  
AAD01124  
ID AAD01124 standard; cDNA; 1173 BP.  
XX AC AAD01124;  
XX DT 02-NOV-2000 (first entry)  
XX DE Human orphan G protein-coupled receptor hRUP7 cDNA.  
XX KW Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening;  
XX KM transmembrane receptor; signal cascade; ss.  
XX OS Homo sapiens.  
XX FH Key  
XX FT 1. .1173  
XX FT /\*tag= a  
XX FT /product= "hRUP7"  
XX FT /note= "Human orphan G protein-coupled receptor"  
XX PN W0200031258-A2.  
XX PD 02-JUN-2000.  
XX PF 13-OCT-1999; 99WO-US023687.  
XX PR 20-NOV-1998; 98US-0109213P.  
XX PR 16-FEB-1999; 99US-0120416P.  
XX PR 26-FEB-1999; 99US-0121852P.  
XX PR 12-MAR-1999; 99US-0123946P.  
XX PR 12-MAR-1999; 99US-0123949P.  
XX PR 28-MAY-1999; 99US-0136436P.  
XX PR 28-MAY-1999; 99US-0136437P.  
XX PR 28-MAY-1999; 99US-0136439P.  
XX PR 28-MAY-1999; 99US-0136567P.  
XX PR 28-MAY-1999; 99US-0137127P.  
XX PR 28-MAY-1999; 99US-0137131P.  
XX PR 29-JUN-1999; 99US-0141448P.  
XX PR 29-SEP-1999; 99US-0156555P.  
XX PR 29-SEP-1999; 99US-0156633P.  
XX PR 29-SEP-1999; 99US-0156634P.  
XX PR 29-SEP-1999; 99US-0156653P.  
XX PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.  
PR 01-OCT-1999; 99US-0157282P.  
PR 01-OCT-1999; 99US-0157283P.  
PR 01-OCT-1999; 99US-0157294P.  
PR 12-OCT-1999; 99US-00416760.  
PR 12-OCT-1999; 99US-00417044.  
XX (AREN-) ARENA PHARM INC.  
XX PI Chen R, Dang HT, Liaw CW, Lin I;  
XX WPI: 2000-400068/34.  
XX P-PSDB; RAY71297.  
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs for  
XX use in the identification of G protein-coupled receptor agonists.  
XX Claim 25; Page 59; 102pp; English.  
XX The present sequence is a cDNA encoding hRUP7, an endogenous human orphan  
XX G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned  
XX by RT-PCR using human peripheral leucocyte cDNA as template. The orphan  
XX GPCR of the invention, like all GPCRs has seven transmembrane alpha  
XX helices with an extracellular N-terminus and an intracellular C-terminus.  
XX However, no endogenous ligands has yet been identified for the proteins  
XX of the invention. The orphan GPCRs may be used in the identification of  
XX their endogenous ligands, and to screen potential GPCR agonists and  
XX antagonists for use as pharmaceutical agents. The proteins may also be  
XX used in the study of GPCR-mediated signalling cascades, and to elucidate  
XX their precise role in normal and diseased human conditions. Nucleic acid  
XX encoding human orphan GPCRs may be used for tissue localisation in  
XX expression analysis to provide information about their function in  
XX healthy and pathological states  
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 3.49e-112 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.3% Conservative: 40  
Best Local Similarity: 68.1% Mismatches: 82  
Query Match: 66.9% Indels: 3  
DB: 3 Gaps: 2  
US-10-626-445-8 (1-391) x AAD01124 (1-1173)  
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20  
Db 1 ATGCCAGTACTAATAGCACAAATCAATTTATCAAGCACTCGTGTGTTAGCATTT 60  
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGAAATGCTTTGGTCATTTAGCTTTT 120  
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAAGTGGCCATCTCT 180  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80  
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACGCTGTTCAATGG 240  
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300  
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 301 TCTGTATATAACATTGTCTCATCATGATGATGATGATGATGATGATGATGATGATGATG 360  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTrp 140  
Db 361 TCTTATAGAACTCAACATATCTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420

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QY 141 ILeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTTCTAGTGAATGGCCAAATGATCTAGTTTCAGAGTCTTGGAAGGATGAA 480
QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrlleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAATGGTACATCCTTGCCATCACA 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaIleTyrllePheAsnValGlnIleTyrl 200
Db 535 TCATCTCTGGAATTCGATGCCAGTCATCTTATAGTCGCTTATTTCAACATGAATATTTAT 594
QY 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCCTGTGGAAAGCGTGATCTCAGTAGGTGCCAAAGCCATCTCGACGACGTGCT 654
QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTCCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTCTCTGTCATCTCTTCAATTCAGAGACAGAGGAGAGAGTAGT 774
QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCCAGAACCAAGATGAATAGCAATCAATTCCTCCAAATATGGGTTC 834
QY 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrlleAlaGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTCTAGTCTCTTCCAAAGGGAACATGTTGAATGCTTAGAGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGCTGTTTGTCTGGGCTCCA 954
QY 321 TyrlleLeuPheThrIleValLeuSerThrTyrlleProArgThrGluArgProLysSerVal 340
Db 955 TATTCTCTGTTCACAAATGTCTTCAATTTATTCCTCAGCAACAGGCTCTTAATCATGTT 1014
QY 341 TrpTyrlleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrl 360
Db 1015 TGGTATAGAAATTCATTTGGCTTCAGTGGTTCATCTCTTGTCAATCTCTTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTACACAGCGCTTTCAAAAGGCTTCTTGAATAATATTTTGTATAAAAAAGCAA 1134
QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTTACCATCACAAACACAGTCGGTCAGTATCTTCT 1170
RESULT 7
AAF83203
ID AAF83203 standard; cDNA; 1173 BP.
XX AAF83203;
AC AAF83203;
DT 09-JUL-2001 (first entry)
XX Human GPCR-like polypeptide, PFI-013 encoding cDNA.
DE
XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;
KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;
KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;
KW signal transduction; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1. 1173
FT CDS /*tag= a
FT

```

```

FT XX EPI096009-A1. /product= "PFI-013"
PN XX
XX 02-MAY-2001.
PD
XX 24-OCT-2000; 2000EP-00309364.
PF 29-OCT-1999; 99GB-00025641.
XX 20-APR-2000; 2000GB-00009973.
PR
XX (PFI2 ) PFIZER LTD.
PA (PFI2 ) PFIZER INC.
XX Peter B, O'reilly MA;
PI WPI; 2001-309854/33.
XX P-PSDB; AAB62445.
DR
XX New G-protein coupled receptor-like polypeptide, polynucleotide for
PT screening drug candidates for treating diseases associated with signal
PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX
XX Claim 1; Page 43; 66pp; English.
PS
CC This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor
CC (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be
CC expressed by standard recombinant methodology. Antibodies and modulators
CC of PFI-013 are useful in the manufacture of a medicament for treating
CC allergic disorder, including extrinsic asthma, immunological disorders,
CC such as intrinsic asthma, vasculitic granulomatous disease, interstitial
CC and other pulmonary disease, including chronic obstructive pulmonary
CC disease (COPD), infectious, inflammatory disease, such as inflammatory
CC bowel disease and neoplastic and myeloproliferative diseases. They are
CC also useful for treating obesity, diabetes, metabolic, neurological
CC diseases, psychotherapeutics, urogenital disease, reproduction and sexual
CC medicine, inflammation, cancer, tissue repair, dermatology, photosaging,
CC skin pigmentation, osteoporosis, cardiovascular, gastrointestinal
CC diseases, allergy and respiratory disease, sensory organ disorders, sleep
CC disorders and hair loss. The PFI-013 protein and nucleic acid are useful
CC in the diagnosis and treatment of the above conditions and also for
CC screening drug candidates for the treatment of diseases associated with
CC signal transduction. The antibodies are also useful for enrichment of
CC eosinophils from mammalian, especially human blood and for detecting the
CC protein in biological samples
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.49e-112 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 4 Gaps: 2

US-10-626-445-8 (1-391) x AAF83203 (1-1173)
QY 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATATGCTAGGAATGCTTTGGTCATTTTAGCTTTT 120
QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAACCACTTAGACATCGAAGTAGTATTTTCTTCACTTGGCCATCTCT 180
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrlleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTCTGGGTGTGATCTCCATCTCTTGTGTACATCCCTCACACGCTGTTCGAATGG 240

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CC useful for diagnosing or determining susceptibility of an individual to a  
 CC disease via the detection of abnormal levels of protein or mRNA, or via  
 CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
 CC also useful for inducing an immunological response in a mammal against  
 CC the above diseases, and for antibody production. AXOR35 nucleotides are  
 CC also useful as diagnostic reagents, in chromosome localisation and tissue  
 CC expression studies, and for producing transgenic animals useful in drug  
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
 CC protein or fragments thereof, and are also useful for treating conditions  
 CC associated with the expression of the AXOR35 protein. The present  
 CC sequence represents cDNA encoding human AXOR35  
 XX  
 SQ

Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3,49e-112 Length: 1173  
 Score: 1370.50 Matches: 267  
 Percent Similarity: 78.3% Conservative: 40  
 Best Local Similarity: 68.1% Mismatches: 82  
 Query Match: 66.9% Indels: 3  
 DB: 5 Gaps: 2

US-10-626-445-8 (1-391) x AAH24007 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20  
 Db 1 ATCCGATACTAATAGACAAATTTATCATAAGCACTCGTGTACTTTAGCATTT 60  
 Qy 21 LeuMetSerPheAlaPheAlaIleMetValGlyAsnValValIleLeuAlaPhe 40  
 Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGTAGGAATGCTTTGTGTCATTTAGCTTTT 120  
 Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 Db 121 GTGGTGACAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGGCCATCTCT 180  
 Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
 Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACGCTGTTGGAATGG 240  
 Qy 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100  
 Db 241 GATTTTGGAAAGGAATCTGTGATATTTTGGTCTACTACTGACTATCTGTTATGTACGCA 300  
 Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATCGATACCTGTGCTCAGTCTCAAAATGCTGTG 360  
 Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140  
 Db 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTGTTACTCTGTATGGTGGCCGTTTGG 420  
 Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160  
 Db 421 GTGCTGGCTCTTCTTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGGAGGATCAA 480  
 Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrPheIleThrIleThr 180  
 Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTTCGGAATGGTATCATCTTGGCCATCACA 534  
 Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
 Db 535 TCATCTTGGAAATTCGGTATCCGAGTCATCTTAGTCGCTTATTTCAACATGAATATTAT 594  
 Qy 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
 Db 595 TGGAGCTGTGGAACGCTGATCATCTCAGTAGTGCCAAAGCCATCTCTGGAGTCACTGCT 654  
 Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
 Db 655 GTCTCTTCCCAACATCTGTGGGACATCTCATTCAGAGGTAGAGTATCTTCAAGAGATCTCTT 714  
 Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260

Db 715 TCTGCATCGACAGAGTCTCTGCATCTCTTCATTCAGAGAGACAGAGGAGAAAGAGTAGT 774  
 Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280  
 Db 775 CTATGTTTTCTTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834  
 Qy 281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
 Db 835 TTCTCCCATCAGATCTGTAGCTCTTCCACCAAGGGAACATGTTGAATGCTTAGAGCC 894  
 Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320  
 Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTTGTCTGGGCTCCA 954  
 Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
 Db 955 TATTCTCTGTTCACAAATTTGTCCTTTCATTTATTCCTCAGCAACAGCTCTTAATCATGTT 1014  
 Qy 341 TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360  
 Db 1015 TGGTATAGATTGCAITTTTGCTTCAGTGTTCATTTCTTGTCAATCCTCTTTTGTAT 1074  
 Qy 361 ProLeuCysHisArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyr 380  
 Db 1075 CCATTGTGTACAGCGCTTTCAAAAGGCTTCTTGAATAATATTTGTATATAAAAGCAA 1134  
 Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391  
 Db 1135 CCTTACCATCACACACACAGCTCGTCTAGTATCTCT 1170  
 RESULT 9  
 ABZ80663  
 ID ABZ80663 standard; cDNA; 1173 BP.  
 XX  
 AC ABZ80663;  
 DT 13-JUN-2003 (first entry)  
 XX Human histamine receptor coding sequence.  
 DE human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;  
 XX anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
 KW anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antipsoriatic;  
 KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
 KW myocardial infarction; migraine; chronic obstructive pulmonary disease;  
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
 KW psoriasis; receptor.  
 XX Homo sapiens.  
 OS  
 PH Key Location/Qualifiers  
 FT CDS 1..1173  
 FT /\*tag= a  
 FT /product= "Histamine receptor"  
 XX  
 PN US6204017-B1.  
 XX  
 PD 20-MAR-2001.  
 XX  
 PF 07-OCT-1999; 99US-00414010.  
 XX  
 PR 07-OCT-1999; 99US-00414010.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;  
 PI Wang S;  
 XX  
 XX WPI; 2002-442063/47.  
 DR P-FSDB; ABO98629.  
 XX  
 XX New nucleic acid encoding antigenic part of human histamine receptor,





XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
 PA Lovenberg T, Liu C;  
 PI WPI; 2002-114339/15.  
 DR P-PSDB; AAM50564.  
 DR  
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 XX Claim 4; Fig 1; 92pp; English.  
 XX  
 CC The present sequence is that of cDNA clone pH4R encoding a human  
 CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone  
 CC marrow cDNA library. The invention provides mammalian (human, mouse, rat  
 CC and guinea pig) histamine H4 receptor nucleic acid molecules (see  
 CC AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have  
 CC been expressed in recombinant host cells that produce active recombinant  
 CC protein. The pharmacology of known histamine ligands is demonstrated.  
 CC Mammalian histamine H4 receptor may be used in gene therapy for the  
 CC treatment of diseases where it is beneficial to elevate mammalian  
 CC histamine H4 receptor activity. Recombinant protein is useful for  
 CC identifying modulators of the human histamine H4 receptor. Such  
 CC modulators may be useful for diagnosing, treating or preventing asthma,  
 CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-  
 CC insulin dependent diabetes mellitus, hyperglycemia, constipation,  
 CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3,49e-112 Length: 1173  
 Score: 1370.50 Matches: 267  
 Percent Similarity: 78.3% Conservative: 40  
 Best Local Similarity: 68.1% Mismatches: 82  
 Query Match: 66.9% Indels: 3  
 DB: 6 Gaps: 2

US-10-626-445-8 (1-391) x AAI70980 (1-1173)

Qy 1 MetSerGluSerAnSerThrGlyIleuProAlaGlnValProLeuAlaPhe 20  
 Db 1 ATGCCAGATACTAATAGCACAAATTTATCTACTAGTACGCTCGTGTACTTAGCATTT 60  
 Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
 Db 61 TTTATGTCCTTAGTAGCTTTTGTATATATGCTAGGAATGCTTGGTCATTTTAGCTTTT 120

Qy 41 ValValAspArgAnLeuArgHisArgSerAsnTyrPhePheLeuAnLeuAlaIleSer 60  
 Db 121 GTGGTGACAAACACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180

Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
 Db 181 GACTTCTTTGTGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTGCAATGG 240

Qy 81 AsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100  
 Db 241 GATTTTGGGAAGGAACCTGTGATTTTGGCTACTACTACTACTACTACTACTACTACTACT 300

Qy 101 SerValTyrAnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATGATGATGATGATGATGATGATGATGAT 360

Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140  
 Db 361 TCTTATAGAACTCAACATCTAGTGGGTCTTGAAGATTCTTCTCTGATGTTGGCGGTTTG 420

Qy 141 IleLeuAlaPheLeuValAnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160  
 Db 421 GTGCTGCCCCTTCTTAGTGAATGGGCCAATGATTTCTAGTCTTCTAGAGTCTTGGAGGATGAA 480

Qy 161 ThrAnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180  
 Db 481 GGTAAGTGAACCTGGATTTTTCGGAATGGTATCATCTTGGCCATCACA 534

Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAnValGlnIleTyr 200  
 Db 535 TCATCTTGGAAATCGTATGCCAGTCACTTAGTCGCTTATTTCACATGAATATTAT 594

Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
 Db 595 TGGAGCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCTGGAGTCTGCT 654

Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAn 240  
 Db 655 GTCTCTTCCAAACATCTGTGGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCT 714

Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgAlaGlySerSer 260  
 Db 715 TCTGCATCGACAGAGTCTCTGCATCTTCAATTCAGAGAGACAGAGAGAGAGAGTAGT 774

Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerIleThrAlaPheLysValGlySer 280  
 Db 775 CTCATGTTTCTCTCAAGAACCAAGATGAATAGCAATACAAATTTGCTTCCAAATGGTTCC 834

Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
 Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGAATCTTGTAGAGCC 894

Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 Db 895 AGGAGATTGCCAAGTCACTGGCCATTTCTTAGGGGTTTTTGTCTTGTCTGGGCTCCA 954

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
 Db 955 TATTCTCTGTTCAAAATTTGCTTTTCAATTTATTTCTCTCAGCAACAGGTCTTAAATCAGTT 1014

Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAnSerPheValAnProPheLeuTyr 360  
 Db 1015 TGGTATAGAAATTCATTTTGGCTTCAAGTGTTCATTTCTTGTCAATCTCTTTTGTAT 1074

Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380  
 Db 1075 CCATTTGTGCACAGCGCTTTCAAAAGCTTTCTTGAAATATATTTTGTATATAAAAGCAA 1134

Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391  
 Db 1135 CCTCTACCATCACACACAGTCGCTCAGTATCTTCT 1170

RESULT 12  
 AAI67750  
 ID AAI67750 standard; cDNA; 1173 BP.  
 XX  
 AC AAI67750;  
 XX  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Human histamine H4 receptor protein encoding cDNA.  
 XX  
 KW Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;  
 KW antiasthmatic; antiallergic; neuroprotective; antidiabetic; human;  
 KW cerebroprotective; cAMP modulator; gene therapy; ss.  
 OS Homo sapiens.  
 PH Key Location/Qualifiers  
 FT CDS 1..1173  
 FT /\*tag= a  
 FT /product= "histamine H4 receptor"  
 XX  
 PN WO200185786-A2.  
 XX  
 PD 15-NOV-2001.







Db 1135 CCTTACCATCACACACAGTCGGTCAGTATCTTCT 1170  
 ||||| ||||| :|||||:|||||:|||||:|||||

## RESULT 14

ADG98759  
 ID ADG98759 standard; cDNA; 1173 BP.

XX AC ADG98759;  
 XX 11-MAR-2004 (first entry)  
 XX Human orphan GPCR cDNA, RUP7.  
 XX Human; G protein-coupled receptor; GPCR; research tool; gene; ss.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 1. 1173  
 FT CDS /\*tag= a  
 FT /product= "Human GPCR protein"  
 FT

XX US2003148450-A1.

XX 07-AUG-2003.

XX 17-OCT-2002; 2002US-00272983.

XX 20-NOV-1998; 98US-0109213P.

XX 16-FEB-1999; 99US-0120416P.

XX 26-FEB-1999; 99US-0121852P.

XX 12-MAR-1999; 99US-0123946P.

XX 12-MAR-1999; 99US-0123949P.

XX 28-MAY-1999; 99US-0136436P.

XX 28-MAY-1999; 99US-0136437P.

XX 28-MAY-1999; 99US-0136439P.

XX 28-MAY-1999; 99US-0137127P.

XX 28-MAY-1999; 99US-0141448P.

XX 28-SEP-1999; 99US-0156333P.

XX 29-SEP-1999; 99US-0156555P.

XX 29-SEP-1999; 99US-0156634P.

XX 12-OCT-1999; 99US-00417044.

XX (CHEN/) CHEN R.

PA (DANG/) DANG H T.

PA (LIAW/) LIAW C W.

PA (LINI/) LIN I.

PI Chen R, Dang HT, Liaw CW, Lin I;

XX WPI; 2003-897571/82.

XX P-PSDB; ADG98760.

PT New cDNA encoding a human G protein coupled receptor, useful for making a  
 PT probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR  
 PT identification of the expression of the receptor in tissue samples.

XX Claim 25; SEQ ID NO 13; 52pp; English.

XX The present invention provides novel human G protein-coupled receptor  
 CC (GPCR) proteins and their encoding nucleic acids. The invention is useful  
 CC for making a probe for dot-blot analysis and for RT-PCR identification of  
 CC the expression of the receptor in tissue samples. The invention is also  
 CC useful for identifying candidate compounds as inverse agonists, agonists  
 CC or partial agonists and as research tools in determining the location of  
 CC the receptors within the body. The present sequence is human orphan G  
 CC protein-coupled receptor cDNA.

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

SQ Alignment Scores:

Pred. No.:	3.49e-112	Length:	1173
Score:	1370.50	Matches:	267
Percent Similarity:	78.3%	Conservative:	40
Best Local Similarity:	68.1%	Mismatches:	82
Query Match:	66.9%	Indels:	3
DB:	10	Gaps:	2

US-10-626-445-8 (1-391) x ADG98759 (1-1173)

Qy	1	MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe	20
Db	1	ATGCCAGATACTAATAGCACAAATTTTACTCTAGCACTCGTGTACTTTAGCAATTT	60
Qy	21	LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe	40
Db	61	TTTATGTCCTTAGTAGCTTTTGTATAATGCTAGGAATGCTTTGGTCATTTAGCTTTT	120
Qy	41	ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTGGTGGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT	180
Qy	61	AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr	80
Db	181	GACTTCTTTGTGGTGTGATCTCCATTCCTTTGTACATCCCTCACGCTGTTGCAATGG	240
Qy	81	AsnPheGlySerGlyIleCysMetPheTyrIleThrAspTyrLeuLeuCysThrAla	100
Db	241	GATTTTGGAAAGGAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA	300
Qy	101	SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCGTATATAACATTGTCTCATCAGCTATGATCGATACCTGTGAGTCTCAAAATGCTGTG	360
Qy	121	SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr	140
Db	361	TCTTATAGAACTCAACATCTCTGGGCTCTCGAAGATTGTTACTCTGATGGTGGCGTTGG	420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrTyrLysAsnSer	160
Db	421	GTGCTGGCCCTCTTAGTAAGTGGCCCAATGATCTAGTTTCAGAGTCTTGGAGGATGAA	480
Qy	161	ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr	180
Db	481	GGTAGT-----GAATGTGAACCTGGATTTTTTTTCGGAATGGTACATCTTGGCCATCA	534
Qy	181	MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr	200
Db	535	TCATTCTTGGAAATTCGGTATGCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT	594
Qy	201	TyrSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr	220
Db	595	TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCTGGACTGACTGCT	654
Qy	221	ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn	240
Db	655	GTCTCTTCCCAACATCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714
Qy	241	ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer	260
Db	715	TCTGCATCGACAGAAAGTTCTCTGCATCTCTTCATTTCAGAGACAGAGAGAGAGTAGT	774
Qy	261	IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer	280
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Qy	301	ArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTyrAlaPro	320
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QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
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 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
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 QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380  
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 Db 1135 CCTTACCATCACAAACAGTCGGTCAGTATCTTCT 1170  
 RESULT 15  
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 ID ABS57063 standard; cDNA; 1173 BP.  
 XX  
 AC ABS57063;  
 XX  
 DT 28-JAN-2003 (first entry)  
 XX  
 DE Human cDNA encoding G-protein coupled receptor AXOR35.  
 XX  
 KW Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;  
 KW macrophage; eosinophil; neutrophil; infection; transplant rejection;  
 KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
 KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
 KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
 KW psoriasis; urological disease; urinary retention; cardiovascular disease;  
 KW myocardial infarction; hypotension; hypertension; pulmonary disorder;  
 KW chronic obstructive pulmonary disease; cough; renal disease;  
 KW renal ischaemia; arteriosclerosis; atherosclerosis; psychosis;  
 KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;  
 KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;  
 KW graft versus host disease; osteoporosis.  
 XX  
 OS Homo sapiens.  
 PH  
 FT Key Location/Qualifiers  
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 FT /\*tag= a  
 FT /product= "AXOR35"  
 XX  
 PN US2002137054-A1.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 20-JUL-2001; 2001US-00910411.  
 XX  
 PR 02-NOV-1999; 99US-00431898.  
 PR 03-FEB-2000; 2000US-00497790.  
 PR 20-OCT-2000; 2000US-00693761.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Aubart KM, Bergsma DJ, Fitzgerald L, Graybill TL, Li X;  
 PI Michalovich D, Morrow DM, Zhu Y;  
 XX  
 XX WPI; 2003-074982/07.  
 DR P-PSDB; ABG71960.  
 XX  
 XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for  
 PT treating infections, gastrointestinal disorders, autoimmune disorders,  
 PT urological diseases, cardiovascular diseases and cancer.  
 XX  
 XX Claim 2; Page 21-22; 24pp; English.  
 XX  
 XX The invention relates to an isolated G-protein coupled receptor  
 CC polypeptide, AXOR35, (and its homologues and variants) and its encoding

CC polynucleotide (and its homologues, variants, complements and RNA  
 CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35  
 CC expression vector, producing a recombinant host cell by introducing the  
 CC vector into a cell such that the host cell produces AXOR35, a membrane of  
 CC the host cell expressing AXOR35, identifying/screening for agonists or  
 CC antagonists of AXOR35 and inhibiting or promoting the function of  
 CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,  
 CC by administering to the patient AXOR35 agonists or antagonists. The  
 CC agonist or antagonist identified is useful for treating a disease such as  
 CC asthma, or for inhibiting or promoting the function of lymphocytes,  
 CC macrophages, eosinophils, or neutrophils in diseased tissue such as an  
 CC achronic lung. AXOR35 or polynucleotide is useful in diagnostic assays,  
 CC for identifying compounds that are agonists or antagonists of AXOR35, as  
 CC vaccines, or for treating infections (bacterial, fungal, protozoan or  
 CC viral infections), transplant rejection, gastrointestinal disorders (such  
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),  
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic  
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,  
 CC psoriasis), urological diseases (such as urinary retention),  
 CC cardiovascular diseases (such as myocardial infarction), hypotension,  
 CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary  
 CC disease), cough, renal diseases (such as renal ischaemia),  
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such  
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft  
 CC versus host disease and osteoporosis. The present sequence is the cDNA  
 CC encoding AXOR35  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
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 Percent Similarity: 78.3% Conservative: 40  
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 DB: 10 Gaps: 2  
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 Db 61 TTTATGTCTCTAGTAGCTTTTGCTATATAATGCTAGGAAATGCTTTGGTCATTTAGCTTTT 120  
 QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 Db 121 GTGGTGGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTGGCCATCTCT 180  
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80  
 Db 181 GACTTCTTTGTGGGTGGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTCGAATGG 240  
 QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
 Db 241 GAATTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTATTGTACGCA 300  
 QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
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 QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140  
 Db 361 TCTTATAGAACTCAACATCTCTGGGCTCTGAGAGATTGTTACTCTGATGGTGGCGCTTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160  
 Db 421 GTGCTGGCTCTCTTAGTGAATGGCCCAATGATCTAGTTTTCAGAGTCTCTGGAAGGATGAA 480  
 QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180

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Db      535  TCATTCTTGGAAATTCGTGATCCCGAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
Qy      201  TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db      595  TGGAGCTGTGGAGCGTGATCATCTCAGTAGGTGCCAAGCCATCCTGGACTGACTGCT 654
Qy      221  ThrSerSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db      655  GTCTCTTCCAACTCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy      241  ProGlyLeuLysGluSerAlaIleSerArgHisSerGluSerProArgArgLysSerSer 260
Db      715  TCTGCATCGACAGAAGTTCCTGCATCTCTTCATTCAGAGACAGAGAGAGAGAGTAGT 774
Qy      261  IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db      775  CTCATGTTTTCCTCAAGAACCAAGATGAATAGCAATACAAATTCCTCCAAAATGGGTTC 834
Qy      281  PheTrpArgSerGluSerAlaIleLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db      835  TTCTCCCAATCAGATCTCTGTAGCTCTTCACCAAGGGAACATGTTGAACCTGTAGAGCC 894
Qy      301  ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
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Qy      361  ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1075  CCATTGTGTCAAGCGCTTTCAAAAGGCTTCTTGAAAAATATTTGTATATAAAAAAGCAA 1134
Qy      381  ProAlaLeuSerGln---AsnGlnSerValSerSer 391
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Search completed: May 25, 2006, 01:50:20  
Job time : 1261 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 25, 2006, 13:51:33 ; Search time 6135 Seconds  
(without alignments)  
5345.833 Million cell updates/sec

Title: US-10-626-445-8

- Perfect score: 2048

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Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -OPMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
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-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abses04  
-USER=US10626445 @CGN 1 1 6323 @runat 24052006 100003 13897 -NCPU=6 -ICPU=3  
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Database : EST:\*

- 1: gb\_est1.\*
- 2: gb\_est3.\*
- 3: gb\_est4.\*
- 4: gb\_est5.\*
- 5: gb\_est6.\*
- 6: gb\_est7.\*
- 7: gb\_est8.\*
- 8: gb\_est9.\*
- 9: gb\_est10.\*
- 10: gb\_est11.\*
- 11: gb\_gses1.\*
- 12: gb\_gses2.\*
- 13: gb\_gses3.\*
- 14: gb\_gses4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	850	41.5	704 5 CF147821	CF147821 AGENCOURT
3	700.5	34.2	2625 6 AK140374	AK140374 Mus muscu
4	482.5	23.6	732 5 CF147822	CF147822 AGENCOURT

5	480	23.4	721	8	CO959034	AGENCOURT
6	456.5	22.3	755	9	DA728518	DA728518
7	453.5	22.1	558	9	DA308555	DA308555
8	432.5	21.1	791	10	DW582260	EST_bsal_
9	429.5	21.0	574	9	DA306992	DA306992
10	423	20.7	542	10	DW576242	EST_bsal
11	416	20.3	728	10	DT257276	JGI_CAAU8
12	415	20.3	672	4	CB556920	AMGNNUC:U
13	413	20.2	2633	6	CR859546	Pongo pyg
14	410	20.2	2967	6	AK138282	Mus muscu
15	410	20.0	3816	6	AK081248	Mus muscu
16	408.5	19.9	853	5	CD326085	AGENCOURT
17	405.5	19.8	3592	6	CR859367	Pongo pyg
18	404.5	19.8	1773	14	AY400782	Homo sapi
19	404	19.7	1770	14	AY400784	Mus muscu
20	404	19.7	3171	6	AK080950	Mus muscu
21	393	19.2	1946	6	AK156130	Mus muscu
22	392	19.1	1764	6	BC018330	Mus muscu
23	392	19.1	2503	6	AK139448	Mus muscu
24	392	19.1	2611	6	AK004891	Mus muscu
25	392	19.1	3050	6	AK043877	Mus muscu
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28	388	18.9	2780	6	AK032763	Mus muscu
29	388	18.9	2831	6	AK047070	Mus muscu
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32	385.5	18.8	1440	14	AY404934	Homo sapi
33	384.5	18.8	1203	14	AY407500	Pan trogl
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36	374	18.3	647	10	DV880423	LB02613.C
37	367.5	17.9	1072	14	AY398880	Homo sapi
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39	365	17.8	1200	14	AY407501	Mus muscu
40	363.5	17.7	1072	14	AY398881	Pan trogl
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ALIGNMENTS

RESULT 1 BX643713 839 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp781C0629\_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone  
DEFINITION DKFZp781C0629 5', mRNA sequence.  
ACCESSION BX643713  
VERSION BX643713.1 GI:34478046  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 839)  
AUTHORS Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Oeanger, A.,  
Fobo, G., Han, M. and Wiemann, S.  
TITLE EST (lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS

MIPS  
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp781C0629) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

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## ORIGIN

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Best Local Similarity: 68.3% Mismatches: 50  
Query Match: 41.8% Indels: 3  
DB: 4 Gaps: 1

US-10-626-445-8 (1-391) x BX643713 (1-839)

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Qy 241 ProGlyLeuLysGluSerAlaAlaSer 249  
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## RESULT 2

CF147821

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 704)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRB102 row: b column: 07

High quality sequence stop: 685.

Location/Qualifiers

1. 704

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/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:

varies by clone; ORFs were PCR-amplified and cloned into

pcDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XmnI/XhoI-3',

5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).

For information about which gene each clones represents,

please visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed\_plates/IRB1.presv.dat

a Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3.85e-75 Length: 704

Score: 850.00 Matches: 165

Percent Similarity: 81.7% Conservative: 27

Best Local Similarity: 70.2% Mismatches: 41

Query Match: 41.5% Indels: 3

DB: 5 Gaps: 1

US-10-626-445-8 (1-391) x CF147821 (1-704)

Qy 3 GluSerAsnSerThrGlyIleLeuProProAlaGlnValProLeuAlaPheLeuMet 22

Db 5 GATACTAATAGCACAAATCAATTTATCATAAGCACTCGTGTCTTAGCAATTTTATG 64

Qy 23 SerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPheValVal 42

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 VERSION AK140374.1  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
 REFERENCE 1 Carninci,P. and Hayashizaki,Y.  
 AUTHORS Carninci,P. and Hayashizaki,Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagasaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,

Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
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 4  
 Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Iehii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,K., I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadoya,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Pezole,G., Quackenbush,J., Schriml,L.M., Staebli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Carninci,P., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawai,J., Kohtsuki,S. and Hayashizaki,Y.  
 RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
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 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Otsu,N., Saito,R., Suzuki,H., Yamana,K., I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Ciothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,D., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Wells,C., Wilming,L.G., Zavalan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kawai,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.  
 FANTOM Consortium  
 Analysis of the mouse transcriptome based on functional annotation  
 Nature 420 (6915), 563-573 (2002)  
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Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Gastin-Hemming, P., Gingers, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huminicki, L., Iacono, M., Ikeo, K., Iwama, K., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kels, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochin, I.V., Lareau, L.P., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuura, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J.F., Reid, J.F., Ring, B.Z., Ringwald, M., Roet, B., Ruan, Y., Salzberg, S.L., Sanderlin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempke, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiyama, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Ye, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hilde, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tonari, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plesky, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J., and Hayashizaki, Y. FANTOM Consortium

**CONSTRM**  
**TITLE** The transcriptional landscape of the mammalian genome  
**JOURNAL** Science 309 (5740), 1559-1563 (2005)  
**PUBMED** 16141072  
**REFERENCE** 7

Katayama, S., Tonari, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sanderlin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B., and Wahlestedt, C.

**CONSTRM**  
**TITLE** RIKEN Genome Exploration Research Group  
**JOURNAL** Antisense transcription in the mammalian transcriptome  
**PUBMED** Science 309 (5740), 1564-1566 (2005)  
**REFERENCE** 16141073  
**AUTHORS** 8 (bases 1 to 2625)

Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A., Muramatsu, M., and Hayashizaki, Y.

**TITLE** Direct Submission  
**JOURNAL** Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

**COMMENT**  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/.

**FEATURES**  
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 732)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
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5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
a Note: this is a NIH_MGC Library."

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US-10-626-445-8 (1-391) x CF147822 (1-732)

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Qy      193 AlaTrpPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAlaLeuSerArgCys 212
Db      412 ACCTTCTTAACTCAGCATCTACTCAACATCCAGAGCGC-----ACCGCCT- 461
Qy      213 ProSerHisAlaGlyPheSerThrThrSerSerAlaSerGlyHisLeuHisArgAla 232
Db      462 CCG-----GCT 467
Qy      233 GlyValAlaCysArgThrSerAsnProGlyLeuLysGluSerAlaAlaSerArgHisSer 252
Db      468 GGATGGGGCTCGAGAGCAGCCGCGCC----- 494
Qy      253 GluSerProArgArgLysSerSerIleLeuValSerLeuArgThrHisMetAsnSerSer 272
Db      495 CGAGCCCTCTCCGAGGCCAGCCCTC-----ACCACC 527
Qy      273 IleThrAlaPheLysVal-GlySerPheTrpArgSerGluSerAlaAlaLeuArgGlnAr 292
Db      528 CCCACCGCTTGGCTGCTGGGCTGCTGCGAGAGGGGCACGCGGAGGCCATGCGCGTSCA 587
Qy      292 gGluTyrAlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSe 312
Db      588 C-----AGAAAGTGGCCAAGTCGTCGCGAGGCGCATGATCATCGGCGCGNCTGCAT 623
Qy      312 rAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrPr 332
Db      624 CATCTTTGGGCTCTGCTGGGCGCCCATACACGCTGCTGATCATCATCGGCGCGNCTGCAT 683
Qy      332 oArgThrGluArgProLysSerValTrpTyr-SerIleAlaPheTrpLeuGlnTrp 350
Db      684 GGGCACTGCTGCCCT---GACTACTGGTACCAAAACCTTCTTCTGCTGCTGCTGCTG 736

RESULT 7
DA308555 558 bp mRNA linear EST 30-OCT-2005
LOCUS DA308555 BRHIP2 Homo sapiens cDNA clone BRHIP2025783 5', mRNA
DEFINITION sequence.
ACCESSION DA308555
VERSION DA308555.1 GI:78290625
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 558)

```

```

AUTHORS Kimura, K., Wakanatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
FEATURES             Location/Qualifiers
     source            1..558
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                     /db_xref="taxon:9606"
                     /clone="BRHIP2025783"
                     /tissue_type="hippocampus"
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                     /notes="Vector: pME18SFL3"
ORIGIN
Alignment Scores:
Pred. No.:          3,94e-35          Length:          558
Score:              453.50           Matches:          93
Percent Similarity: 65.6%            Conservative:    25
Best Local Similarity: 51.7%         Mismatches:      53
Query Match:        22.1%            Indels:          9
DB:                  Gaps:           3

US-10-626-445-8 (1-391) x DA308555 (1-558)
Qy      18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db      26 CTGCGCGCTCATGGCGCTGCTCATGTCGCCACGCTGTGGGCAACGCGTGTGTCATG 85
Qy      38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db      86 CTGCGCTTCGTGGCGGACTCGAGCTCCGCCACCCAGAACAACTTCTTCTGCTCAACCTC 145
Qy      58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db      146 GCCATCTCCGACTTCTCTGTCGGGCGCTTCTGATCCCTGATGATGATACCTGCTGCTG 205
Qy      78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db      206 ACAGGCGCTGGACCTTCGCGCGGCGCTCTGCAAGCTGTGGCTGTGTAGTGACTACCTG 265
Qy      97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db      266 CTGTGCACTCTCTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTCTGCTGCTG 325
Qy      117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValIleAlaGlnMet 136
Db      326 ACCGAGCGGTCTCATACCGGCGCCAGCAGGGTGACACGCGCGCGGAGTGCAGGAATG 385
Qy      137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db      386 CTGCTGTGTGGTGTGGCTTCTCTGCTGTACGGACCGACCTCTG-----AGC 436

```

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QY 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
    |||:::
Db 437 TGGAGTACTGTCGGGGCAGCTCCATCCCGAGGCCACTGCTATGCGGAGTTCTTC 496
    |||:::
QY 172 ThrGluTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp 191
    |||:::
Db 497 TACAACGTGGTACTCTCTCATCAGCGCTCCACCGCTGGAGTCTCTTACGCCCTTCTCCTCAGC 556
    |||:::

RESULT 8
DW582260 791 bp mRNA linear EST 17-JAN-2006
EST ssal rgb2 46679 rgb2 Salmo salar cDNA clone
ssal rgb2_575_176_rev 5', mRNA sequence.

ACCESSION DW582260
VERSION 1
KEYWORDS
SOURCE
ORGANISM Salmo salar (Atlantic salmon)

REFERENCE
AUTHORS Koop,B.F., Davidson,W.S. and cGRASP Consortium.
TITLE Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
JOURNAL
COMMENT Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.
Marra. Bioinformatics: Centre for Biomedical Research, University
of Victoria Jong Leong, BF Koop.
Insert Length: 791 Std Error: 0.00
Plate: 575
Seq primer: M13 Reverse
High quality sequence stop: 791.
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1. .791
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/clone_lib="rgb2"
/notes="Organ: brain, kidney, spleen; Vector: pCMVSPORT6;
ssalrgb2 mixed tissue Salmo salar cDNA; Tissue
contributors: Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN
Alignment Scores:
Pred. No.: 9,26e-33 Length: 791
Score: 432.50 Matches: 91
Percent Similarity: 63.4% Conservative: 32
Best Local Similarity: 46.9% Mismatches: 62
Query Match: 21.1% Indels: 10
DB: 10 Gaps: 3

US-10-626-445-8 (1-391) x DW582260 (1-791)

QY 8 GlyIleLeuProAlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPhe 27
    |||:::
Db 220 GGACAAATCTCTCGCTACCTCGTCTTCTGGCTGTGCTCATGATGCTTCTTGTCTTC 279
    |||:::
QY 28 AlaIleMetValGlyAsnAlaValAlaIleLeuAlaPheValValAspArgAsnLeuArg 47
    |||:::
Db 280 GCCACTGTGTAGCAACGCGCTTGTAATCTAGCCCTTCGGTGGAGAAAGTTCCGA 339
    |||:::
QY 48 HisArgSerAsnTrpPhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIle 67
    |||:::

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Db 340 ACTCAAGGGAACATTTTCTTTTGAATTTGGCCATAGCCGATTTACTCGTTGGAGGTTTT 399
    |||:::
QY 68 SerIleProLeuTyrlleProHisValLeuPhe---AsnTrpAsnPheGlySerGlyIle 86
    |||:::
Db 400 TGTATTTCCGGTTTATATCCCTATGTCATTTACCGGCGAGTGGAGACTCGGACGAGTCTT 459
    |||:::
QY 87 CysMetPheTrpLeuIleThrAspTrpLeuLeuCysThrAlaSerValTrpAsnIleVal 106
    |||:::
Db 460 TGCAGATATGGCTGGTGGTGGACTATATTTATGCACTGCATCAGTGTTCACATCGTC 519
    |||:::
QY 107 LeuIleSerTrpAspArgTrpGlnSerValSerAsnAlaValSerTrpArgAlaGlnHis 126
    |||:::
Db 520 CTGATCAGCTTCGACAGATTTATATCTGTACACAACGCGTGAGCTACAGGTCTCAGAAA 579
    |||:::
QY 127 ThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal 146
    |||:::
Db 580 GGTGTGACCGGAGGCTGTTCTGAAGATGATGAGTGTGGCTGGCTGTTTCTTACTC 639
    |||:::
QY 147 AsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThr----- 163
    |||:::
Db 640 TATGGCCCGCAGCATATATC-----TGGAGTACATTCCTGGTAGTGTGGTG 690
    |||:::
QY 164 -----LysAspCysGluProGlyPheValThrGluTrpTrpTrpTrpTrpTrp 181
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Db 691 CCCGACAAAAGAGTGCACGCTGAGTTTACTTCAACTGGTATTTCTTGATGACAGCATCC 750
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QY 182 LeuLeuGluPheLeuLeuProValIleSerValAlaLysPhe 195
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Db 751 ACTGTAGAGTTTTC-ACCCCTTTGTATTGTCATGTACTTC 791
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RESULT 9
DA306992 574 bp mRNA linear EST 28-OCT-2005
DA306992 BRHIP2 Homo sapiens cDNA clone BRHIP2023706 5', mRNA
sequence.
ACCESSION DA306992
VERSION 1
KEYWORDS GI:78244614
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 574)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Teuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuna,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanabe,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
FEATURES
source
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/clone="BRHIP2023706"  
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## ORIGIN

Alignment Scores:  
Pred. No.: 1.12e-32 Length: 574  
Score: 429.50 Matches: 86  
Percent Similarity: 64.7% Conservativity: 24  
Best Local Similarity: 50.6% Mismatches: 51  
Query Match: 21.0% Indels: 9  
DB: 9 Gaps: 3

US-10-626-445-8 (1-391) x DA306992 (1-574)

Qy 46 LeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuValGly 65  
Db 1 CTCGGCACCAGACAACTTCTCTGCTCAACTCGCCATCTCGACTTCTCTGGC 60  
Qy 66 LeuLeuSerIleProLeuTyrIleProHisValLeuPhe---AsnTrpAsnPheGlySer 84  
Db 61 GCCTTCTGCATCCCACTGTATGTAACCTACGTGTGACAGCGCGCTGGACCTTCGGCGG 120  
Qy 85 GlyIleCysMetPheTrpLeuLeuThrAspTyrIleLeuLeuCysThrAlaSerValTyrAsn 104  
Db 121 GGCCTCTGCAAGCTGTGGTGTAGTGAGTACCTGCTGTGTGACCTCTCTGCCCTTCAAC 180  
Qy 105 IleValLeuLeuSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAla 124  
Db 181 ATCGTGTCTACATCAGTACGACCGCTTCTGTGCTCACCGAGCGGTCTCATACCGGCC 240  
Qy 125 GlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPhe 144  
Db 241 CAGCAGGCTGACACGCGCGGCGAGTGGGAAGATGTGCTGTGGTGTGGCTGCTGCCTC 300  
Qy 145 LeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLys-----Asn 159  
Db 301 CTGCTGTACGAGCAGCAGCATCTCTG-----AGCTGGGAGTACCTGTCCGGGGGCGAGC 351  
Qy 160 SerThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTrpTyrIleLeuThrIle 179  
Db 352 TCCATCCCGAGGGCCACTGTATGCGAGTCTTCTACAACTGGTACTTCTCATCAGC 411  
Qy 180 ThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaIlePheAsnValGlnIle 199  
Db 412 GCTTCCACCTGGAGTCTTTACGCCCTCTCTCAGCGTCACTTCTTTAACTCAGCATC 471  
Qy 200 TyrTrpSerLeuTrpLysArgArgAlaLeu 209  
Db 472 TACCTGAACATCCAGCGGCGCACCGGCTC 501

## RESULT 10

DW576242 542 bp mRNA linear EST 17-JAN-2006  
LOCUS EST ssal\_rgb2\_40661\_rgb2\_Salmo\_salar\_cDNA\_clone  
DEFINITION ssal\_rgb2\_566\_015\_rev\_5', mRNA sequence.

ACCESSION DW576242.1 GI:85048064

## KEYWORDS

Sermo (Atlantic salmon)

## ORGANISM

Salmo salar  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

## REFERENCE

1 (bases 1 to 542)  
Koop,B.F, Davidson,W.S. and cGRASP Consortium.  
Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)  
JOURNAL Unpublished (2006)

## COMMENT

Contact: Koop BF  
Centre for Biomedical Research  
University of Victoria  
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada

Tel: 250 472 4067  
Fax: 250 472 4075  
Email: bkoop@uvic.ca  
Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.  
Marra. Bioinformatics: Centre for Biomedical Research, University  
of Victoria Jong Leong, BF Koop.  
Insert Length: 542 Std Error: 0.00  
Plate: 586  
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High quality sequence stop: 542.  
Location/Qualifiers  
1. -542  
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/clone\_lib="rgb2"  
/notes="Organ: brain, kidney, spleen; Vector: pCMVSPORT6;  
ssalrgb2 mixed tissue Salmo salar cDNA; Tissue  
contributors: Robert Devlin (DFO, Vancouver, B.C.)"

## FEATURES

source

## ORIGIN

Alignment Scores:  
Pred. No.: 4.63e-32 Length: 542  
Score: 423.00 Matches: 90  
Percent Similarity: 64.7% Conservativity: 22  
Best Local Similarity: 52.0% Mismatches: 51  
Query Match: 20.7% Indels: 10  
DB: 10 Gaps: 4

US-10-626-445-8 (1-391) x DW576242 (1-542)

Qy 45 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuVal 64  
Db 1 AGCCTAGCAATCAAGCACTACTTCTTCTCAACCTTGCCATTCAGATTTCTTGT 60  
Qy 65 GlyLeuLeuSerIleProLeuTyrIleProHisValLeuPhe---AsnTrpAsnPheGly 83  
Db 61 GGTGCATTCGTATCCCTGTATATACCTTACCACTCCCTGACAGCGCGCTGGTGGGC 120  
Qy 84 SerGlyIleCysMetPheTrpLeuLeuThrAspTyrIleLeuLeuCysThrAlaSerValTyr 103  
Db 121 AGAGGTCTCTGTAAAGCTGTGGCTCTCATGAGTACTTGTCTGCACCTGCTGTCTTC 180  
Qy 104 AsnIleValLeuLeuSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArg 123  
Db 181 AACATAGTCTCTATCAGCTATGACCGTTCTCTCCGTCCACGAGCAGTGAATATAGA 240  
Qy 124 AlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAla 143  
Db 241 GCTCAGCGGAGCATGCCACCACCATGCTGTGTGAAGATGGTGGTGTGGTGGTGGC 300  
Qy 144 PheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrp-----Lys 158  
Db 301 TTCCTTCTCTATGGCCCTGCGCATTCATC-----TTCTGGGAGCTGGTTTGGGTAAA 351  
Qy 159 AsnSerThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTrpTyrIleLeuThr 178  
Db 352 AGCATCTCTCGCCGAGAGTGTTCGCTGAGTCTTACTGCACCTGGTACTTCTCTATC 411  
Qy 179 IleThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaIlePheAsnValGln 198  
Db 412 AGTGGCTACGTTTGAGTTCTTCCACCCCTTTATCTCTGTGACCTTCTTCAACCTGTGC 471  
Qy 199 IleTyrTrpSerLeuTrpLysArgArgAlaLeuSerArg 211  
Db 472 ATCTACCTGACATC---CAGAGGAGGAGCAAGAGCAGG 507

## RESULT 11

DW576242 728 bp mRNA linear EST 18-AUG-2005  
LOCUS DT257276

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DEFINITION JGI CAU08039.fwd CAU Pimephales promelas brain 7-8 month adults,
males and females pooled (L) Pimephales promelas cDNA clone
CAU08039 5', mRNA sequence.
VERSION DT257276.1 GI:73559225
SOURCE EST.
ORGANISM Pimephales promelas
Pimephales promelas
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Pimephales.
1 (bases 1 to 728)
Richardson, P., Lucas, S., Rokhsar, D., Dettter, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Pimephales promelas EST project
Unpublished (2005)
Other ESTs: JGI CAU08039.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
CDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CAU0801 row: n column: 18
High quality sequence stop: 706.
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location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:90988"
/clone="CAU08039"
/tissue_type="brain"
/clone_lib="CAU Pimephales promelas brain 7-8 month
adults, males and females pooled (L)"
/notes="vector: pCMVSPORT6; The library was made from dt
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Poly A RNA were primed with an oligo dt primer (5'-
GACTAGTTCTAGTCGCGACGCGCGCCCTTTTCTTTT-3') ligated
to a SalI adapter (5'- TCACCCACGCGTCG and 5'-
CGGACGCGTGGG) and digested with NotI. cDNA was size
selected using 1.1% agarose gel electrophoresis (L
-0.5-1.2k, M -1.2-2.5k, H ->2.5k) then ligated into NotI
and SalI digested pCMVSPORT6 vector. The work was done at
DOE Joint Genome Institute."
ORIGIN
Alignment Scores:
Pred. No.: 3.81e-31 Length: 728
Score: 416.00 Matches: 81
Percent Similarity: 71.9% Conservative: 29
Best Local Similarity: 52.9% Mismatches: 39
Query Match: 20.3% Indels: 4
DB: 10 Gaps: 2
US-10-626-445-8 (1-391) x DT257276 (1-728)
Qy 8 GlytLeuProAlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPhe 27
Db 257 GGCCAGTTTACTCCATCCACCTCAATATTCCTGACAGTTCTCATGACACTGCTGGTGTTC 316
Qy 28 AlaLeuMetValGlyAsnAlaValValLeuAlaPheValAlaPheValAsnLeuArg 47
Db 317 GCCACGGTTCGCGAAGCCGCTGTGATTTTGTAGCTTTTGGTGGAGAAAGTTTACGC 376
Qy 48 HisArgSerAsnTyrPhePheLeuAsnLeuAlaLeuSerAspPheLeuValGlyLeu 67

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```

Db 377 ACACAGGCAACTTTTCTTTTAAATTTGGCCATAGCGGACTTCTTGTGCGTGGGTTT 436
Qy 68 SerLeuProLeuTyrIleProHisValLeuPhe---AsnTrpAsnPheGlySerGlyIle 86
Db 437 TGCATCCCCGTATATTCCTATGCTCCTGACGGGTGAGTGGAGGCTGGGAGAGGCTG 496
Qy 87 CysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleVal 106
Db 497 TGTAACCTGTGGCTGGTGGTGGATTACATGTTGTGCACTGCTCAGTCTTCAACATCGT 556
Qy 107 LeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGlnHis 126
Db 557 CTCATCAGTTTCGACAGGTTTCAGTCCGTCATCAAAAGCGGTGAGTTACCATTTGCCAAAG 616
Qy 127 ThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal 146
Db 617 GGGATCACACAGAGAGGCTGTTTGAAGATGCTCTGTGTGGCTTGCAGCGTTCCTCTT 676
Qy 147 AsnGlyProMetIleLeuAlaSerAspSerTrpLysAsn 159
Db 677 TATGTCACGCGATTATC-----AGTTGGGAACAC 706
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CB556920
LOCUS
DEFINITION CB556920 672 bp mRNA linear EST 02-APR-2003
AMGNMUC:URGP1-00001-d6-A urgp1 (14349) Rattus norvegicus cDNA clone
CB556920
ACCESSION CB556920
VERSION CB556920.1 GI:29496320
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 672)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
FEATURES
source
location/Qualifiers
1..672
/organism="Rattus norvegicus"
/mol_type="mRNA"
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/clone="urp1-00001-d6"
/clone_lib="urgp1 (14349)"
/notes="vector: pSPORT1; Rat GPCR library rearranged
internal pSPORT vector"
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Alignment Scores:
Pred. No.: 4.23e-31 Length: 672
Score: 415.00 Matches: 82
Percent Similarity: 73.2% Conservative: 22
Best Local Similarity: 57.7% Mismatches: 34
Query Match: 20.3% Indels: 4
DB: 4 Gaps: 2
US-10-626-445-8 (1-391) x CB556920 (1-672)
Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaLeuMetValGlyAsnAlaValIle 37
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 The German cDNA Consortium  
 TITLE Direct Submission  
 JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764  
 Neuherberg, GERMANY  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by BMFZ (Biomedical Research Center at the  
 Heinrich-Heine-University, Duesseeldorf/Germany) within the cDNA  
 sequencing consortium of the German Genome Project. This clone  
 (DKFZp459P0517) is available at the RZPD Deutsches  
 Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
 Please contact RZPD for ordering:  
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459P0517  
 Further information about the clone and the sequencing project is  
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 High-efficiency full-length cDNA cloning  
 Mech. Enzymol. 303, 19-44 (1999)  
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 and Hayashizaki, Y.  
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 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
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US-10-626-445-8 (1-391) x AK081248 (1-3816)

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GenCore version 5.1.8  
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Database : Issued Patents NA.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/pp COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1370.5	66.9	1173	3	US-09-812-216-1
3	1370.5	66.9	1173	3	US-09-875-076-13
4	724.5	35.4	2665	3	US-09-949-016-5059
5	724.5	35.4	2689	2	US-08-985-090-1
6	724.5	35.4	2689	3	US-09-165-543-1
7	724.5	35.4	2699	3	US-09-167-354-5
8	724.5	35.4	2699	3	US-09-642-855-5

9	724.5	35.4	2699	3	US-09-642-514-5	Sequence 5, Appli
10	724.5	35.4	2699	3	US-09-642-852-5	Sequence 5, Appli
11	722.5	35.3	1335	2	US-08-985-090-3	Sequence 3, Appli
12	722.5	35.3	1335	3	US-09-165-543-3	Sequence 3, Appli
13	722.5	35.3	1335	3	US-09-167-354-6	Sequence 6, Appli
14	722.5	35.3	1335	3	US-09-642-855-6	Sequence 6, Appli
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16	722.5	35.3	1335	3	US-09-642-852-6	Sequence 6, Appli
17	722.5	35.3	2050	3	US-09-891-053-21	Sequence 21, Appli
18	716.5	35.0	1338	3	US-09-165-543-6	Sequence 6, Appli
19	716.5	35.0	1953	3	US-09-891-053-26	Sequence 26, Appli
20	716.5	35.0	3244	3	US-09-165-543-4	Sequence 4, Appli
21	709.5	34.6	1239	3	US-09-891-053-2	Sequence 2, Appli
22	709.5	34.6	2700	3	US-09-891-053-5	Sequence 5, Appli
23	624.5	30.5	1056	3	US-09-524-162-1	Sequence 1, Appli
24	582.5	28.4	1086	2	US-08-985-090-6	Sequence 6, Appli
25	582.5	28.4	1086	2	US-09-165-543-33	Sequence 33, Appli
26	582.5	28.4	2218	2	US-08-985-090-4	Sequence 4, Appli
27	582.5	28.4	2218	3	US-09-165-543-31	Sequence 31, Appli
28	415.5	20.3	1956	2	US-08-313-553-6	Sequence 6, Appli
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30	413	20.2	1386	3	US-09-016-434-1339	Sequence 1339, Ap
31	413	20.2	1522	5	US-09-543-679A-2589	Sequence 2589, Ap
32	413	20.2	6707	5	US-09-543-679A-2593	Sequence 2593, Ap
33	408	19.9	1422	3	US-09-826-509-512	Sequence 512, App
34	404.5	19.8	1913	3	US-09-016-434-1314	Sequence 1314, Ap
35	404.5	19.8	1913	5	US-09-543-679A-2592	Sequence 2592, Ap
36	404.5	19.8	2261	3	US-09-016-434-1176	Sequence 1176, Ap
37	401	19.6	1893	3	US-09-891-053-13	Sequence 13, Appl
38	401	19.6	9293	3	US-09-949-016-16801	Sequence 16801, A
39	399.5	19.5	1599	3	US-09-826-509-520	Sequence 520, App
40	399.5	19.5	1773	3	US-09-826-509-516	Sequence 516, App
41	393	19.2	1581	2	US-08-313-553-8	Sequence 8, Appli
42	393	19.2	1581	2	US-08-767-993-8	Sequence 8, Appli
43	392	19.1	1621	2	US-08-722-001-13	Sequence 13, Appl
44	392	19.1	2002	3	US-09-016-434-1172	Sequence 1172, Ap
45	390	19.0	1776	2	US-08-722-001-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-09-414-010-1  
; Sequence 1, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414.010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-414-010-1

Alignment Scores:  
Pred. No.: 5.57e-133 Length: 1173  
Score: 1370.5 Matches: 267  
Percent Similarity: 78.3% Conservative: 40  
Best Local Similarity: 68.1% Mismatches: 82  
Query Match: 66.9% Indels: 3  
DB: 3 Gaps: 2

US-10-626-445-8 (1-391) x US-09-414-010-1 (1-1173)

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Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCATAAGCACTCGTGTACTTTAGCAATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCAATTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTATATTTTCTTAACCTTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTTGTGGGTGTGATCTCATTTCTTTGTACATCCCTCACAGCTGTTTGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuAlaIleSer 100
Db 241 GATTTTGGAAAGGAATCTGTATTTTGGTCTACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATCGATACCTGTCAAGTCTCAAAATGCTGTG 360
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Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
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Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
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## RESULT 2

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US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1
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Alignment Scores:
Pred. No.: 5,57e-133 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: Gaps: 2
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US-10-626-445-8 (1-391) x US-09-812-216-1 (1-1173)

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RESULT 3
US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
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; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Alignment Scores:
Pred. No.: 5,57e-133 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: Gaps: 2

US-10-626-445-8 (1-391) x US-09-875-076-13 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATCCGATAGTAAATAGCACAAATCAATTTATCTAGTACTCGTGTACTTAGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTCTAGTAGCTTTTGTCTATAATCTAGGAAATGCTTTGGTCATTTAGCTTTT 120
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Db 181 GACTCTTTGTGGGTGATCTCCATCTCTTTGTACATCCCTCACAGCTGTTCGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATTGTACGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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Db 361 TCTTATAGAACTCAACATCTCGGGTCTGAAGATTTCTACTCTGATGGTGGCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTAATGGCCCAATGATCTTAGTTTCAGAGCTCTTGAAGGATGAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTGCCATCACA 534
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
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Db 595 TGGAGCTGTGGAAGCGGTGATCATCTCAGTAGTGCCAAAGCCATCTCTGAGCTGACTGCT 654
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
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Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTCTGGGCTCCA 954
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## RESULT 4

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US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059

Alignment Scores:
Pred. No.: 5,6e-65 Length: 2665
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 3 Gaps: 12
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US-10-626-445-8 (1-391) x US-09-949-016-5059 (1-2665)
Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle 37
Db 400 CTGCCCGCTCATGGCGCTGCTCATCTGTCGCCACCGTGTGGCAACGGCTGTCTCATG 459
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 460 CTGCCCTCTCGTGGCGACTCGAGCCTCGCACCCAGAACAACTTCTTCTCTGCTCAACCTC 519
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIle 77
Db 520 GCCATCTCCGACTTCTCTGTCGGCGCTTCTGTACCTCCACTGTATGACCTACGTGCTG 579
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 580 ACAGGCGCTGGACCTTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTACTACTGCTG 639
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 640 CTGTGCACCTCTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTCTCGCTC 699
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 700 ACCCGAGCGTCTCATACCGGGCCAGCAGGGTGACACGGCGGGCGAGTGGCGGAATG 759
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 760 CTGCTGTGTGGGTGCTGGCTTCTCTGTGTACGGACCGACCATCTCTG-----AGC 810
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 811 TGGGAGTACCTGTCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGAGTCTTTC 870
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 871 TACAACCTGGTACTTCTCTCATCAGCGCTTCCACCTGTGAGTTCTTTTACGCCCTTCTC 930
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 931 GTACCTTCTTAACTTACCTCAGCATCTACTGAACATCCAGAGGCGCACCCGCTCGGGCTG 990
Qy 200 ----- 200
Db 991 GATGGGCTCGAGAGGCGAGCGGCCCGAGGCCCTTCCGAGGCCCGAGCCCTCACCACCC 1050
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 1051 CCACCGCTGTGCTGTGGGCTGTCTGGCAGAAAGGGGCAACGGGAGGCCATCGCTGCAC 1110
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1111 AGGTATGGGTGGGTGAGGGCGGCGTAGGCGCTGAGGCGCGGGGAGGCGCACCTCGGGGT 1170
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Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1171 GCGCGTGGGGC-----GGCTCCGCTGCCTACCCAGCTCCAGCTCCGGC--- 1215
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1216 -----AGCTCTCGAGGGGCACTGAGAGCGCGGC----- 1245
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 1246 -----TCACTCAAGAGGGGCTCCAGCCGCTCG 1272
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1273 GCGTCTCGGCGCTCACTGGAGAACGCGATGAGTGTGCCAGAGCTTCACCCAGCGC 1332
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1333 TTTCGGCTGTCTCGGCACAGAAAGTGGCAAGTGGTGGCCGTCATCGTGAGGATCTTT 1392
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1393 GGGCTCTGTGGGCCCCATACACGCTGCTGATGATCATCGGGCGCGCTGCCATGGCCAC 1452
Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1453 TGCCTCCCT---GACTACTGGTACGAAACCTCTTCTGGCTCTGTGGGCCAACTCGGCT 1509
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1510 GTCAACCTGTCTTACCTCTGTGTCACACACAGCTTCGCCGGGCTTCACCAAGCTG 1569
Qy 375 LeuCysValThrLys-----Trp----- 380
Db 1570 CTCTGCCCCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGAAGTGA 1629
Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1630 GTGGCCCCCAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCAGGCTCT 1677

RESULT 5
US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/985,090
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
```

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-08-985-090-1

Alignment Scores:
Pred. No.: 5.68e-65 Length: 2689
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 2 Gaps: 12

US-10-626-445-8 (1-391) x US-08-985-090-1 (1-2689)
Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle 37
Db 399 CTGGCCGCGCTCATGGCGCTGCTCATCGGCCACGGTGTGGGCAACGCGCTGGTCATG 458
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 459 CTGCGCTTCGTGGCGGACTCGAGCCTCGGCACCCAGAACAACTTCTTCTCTCAACCTC 518
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 519 GCCATCTCCGACTTCTCTCGCGCGCTTCTGCATCCCACTGTATGATACCTACGTGCTG 578
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 579 ACAGCCGCTGGACCTTCGCGCGGCGCTCTGCAGGCTGTGGTGTGTAGTACTACCTG 638
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 639 CTGTGACCTCTCTGCTTCAACATCGTGTATCATAGTACGACCGCTTCTCTCGGTC 698
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 699 ACCGAGCGGTCTCATACCGGGCCGACAGGGTGACACGGCGCGGCGAGTCCGGAAGATG 758
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 759 CTGCTGTGTGGGTGTGGCTTCTCTGTCTGACGACCGACCATCTCTG-----AGC 809
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 810 TGGAGTACCTGTCCGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGAGTCTTC 869
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 870 TACAACCTGGTACTTCTCTCATCAGCGCTTCCACCCCTGGAGTCTTTTACGCCCTCTC 929
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 930 GTCACTTCTTTTAACTCTCAGCATCTACCTGAACATCCAGAGGGCGACCCGCTCGGCTG 989
Qy 200 ----- 200
Db 990 GATGGGCTCGAGAGGCGAGCGCGCCCGAGCCCTCCCGAGGGCCAGCCCTCACCACCC 1049
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 1050 CCACCGCTCGCTGCTGGGCTGTCTGCGAGAAGGGGCAACCGGGAGGCCATCCCGCTGC 1109
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1110 AGGTATGGGTGGGTGAGGGCGCGCTAGGCGCTGAGCGCGGGAGGAGCGACCTCGGGGT 1169
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QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1170 GCGCGTGGGGC-----GGCTCGCTGGCTTCAACCACCTCCAGTCCGGC--- 1214
QY 244 LysGluSerAlaAspArgHisSerGluSerProArgArgIysSerSerIleLeuVal 263
Db 1215 -----AGCTCTCGAGGGCACTGAGAGCGCGGC----- 1244
QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySerPheTrpArg 283
Db 1245 -----TCACTCAAGAGGGCTCCAAAGCCGTG 1271
QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1272 GCGTCTCGGCTCAGCTGGAGAACGCGATGAGATGGTGTCCAGAGCTTCACCCAGCGC 1331
QY 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1332 TTTCCGGCTGTCTCGGGACAGAAAGTGGCCAAAGTCGCTGGCGGTCACTCGTGAGCATCTTT 1391
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1392 GGGCTCTGCTGGGCCCATACACCTCTGATGATCATCCGGCGCCGCTGCCATGGCCAC 1451
QY 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1452 TGCCTCCT---GACTACTGTGATGAAACCTCTCTTGCTCTCTGTGGGCCAATCGGCT 1508
QY 355 ValAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1509 GTCAACCTGTCTCTACCTCTGTGCCACACAGCTTCGCGCGGCTTCACCAAGCTG 1568
QY 375 LeuCysValThrLys-----Trp----- 380
Db 1569 CTCTGCCCCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGTGTGAAGTGA 1628
QY 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1629 GTGCCCCCAGAGCTCCCTTCAGCCACAGCCTCTCTCAGCCCCAGGTCT 1676

RESULT 6
US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-09-165-543-1

Alignment Scores:
Pred. No.: 5,68e-65 Length: 2689
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: Gaps: 12

US-10-626-445-8 (1-391) x US-09-165-543-1 (1-2689)
QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle 37
Db 399 CTGCGCGCTCATGGCGTCTCATCTGGCCACGGTGTGGGCAACGGCGCTGTCATG 458
QY 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 459 CTGCGCTTCGTGGCGGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTC 518
QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIle 77
Db 519 GCCATCTCCGACTTCTCTCGTCGGCGCCTTTCGATCCACCTGATGATGATGATGATG 578
QY 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIle 96
Db 579 ACAGGCGCTGGACCTTCGGCGCGGGCTCTGCAAGCTGTGGTGGTAGTGGACTACCTG 638
QY 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 639 CTGTGCACCTCCTCTGCTTCAACATCGTCTCATACAGCTACGACCCCTTCTCTCGGTC 698
QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 699 ACCGAGCGGTCTCATACCGGGCCACAGCGGTGACACGGCGGGGCGGAGATG 758
QY 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 759 CTGCTGTGTGGTGTCTGCTGCTGCTGTACGACGACGACATCTG-----AGC 809
QY 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 810 TGGGAGTACCTGTCCGGGGCGAGCTCCATCCCGAGGGCCACTCTGCTATGCCGAGTTCTTC 869
QY 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuValIleSer 191
Db 870 TACAACCTGGTACTCTCTCATCAGCGCTTCACCCCTGGAGTCTTTACGCCCTTCTCTCAGC 929
QY 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 930 GTCACCTTCTTTAACCTCAGCATCTACGTGAACATCCAGAGGGCGACCCGCTCCGGCTG 989
QY 200 ----- 200
Db 990 GATGGGCTCGAGAGGAGCGGGCCCGAGCCCTCCCGAGGGCCCGCTCCACCCC 1049
QY 201 -----TrpSerLeuTyrPlyArgArgAlaLeuSerArgCysProSerHis 215
Db 1050 CCACCGCTGGCTGCTGGGGCTGCTGCGACAGAGGGGCGGAGGAGCCATCCCGCTGCAC 1109
QY 216 -----AlaGlyPheSerThrThrSerSer 223
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Db      1110 AGGTATGGGTGGGTGAGCGCGCGTAGGCGCTGAGCGCGGAGGCGACCTCGGGGGT 1169
Qy      224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db      1170 GCGCGTGGGGC-----GGCTCCGTGGCTTCAACCCACTCCAGCTCCGGC--- 1214
Qy      244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db      1215 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 1244
Qy      264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db      1245 -----TCACTCAAGAGGGGCTCAAGCCGTCG 1271
Qy      284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db      1272 GCGTCTCGGCTCACTCGAAGAGCGCATGAAGATGGTGTCCAGAGCTTCAACCAGCGC 1331
Qy      295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaLleLeuLeuSerAlaPhe 314
Db      1332 TTTCGGCTGTCTCGGACAGAAAGTGGCCAAAGTCGCTGGCCGTCATCGTGAGCATCTTT 1391
Qy      315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db      1392 GGGCTGTCTGGGCCCCATACACGCTGCTGATGATCATCCGGCGCGCTGCCATGGCCAC 1451
Qy      335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db      1452 TGCCTCCCT---GACTACTGTGACAAACCTCTCTGGCTCTCTGGCCCACTCGGCT 1508
Qy      355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db      1509 GTCAACCTGTCTCTACCTCTGTGCCACACAGCTTCCGCGCGGCTTCAACCAAGCTG 1568
Qy      375 LeuCysValThrLys-----Trp----- 380
Db      1569 CTGTGCCCCCAGAGCTCAAAATCCAGCCACAGCTCCCTGGAGCACTGCTGAAGTGA 1628
Qy      381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db      1629 GTGGCCACCAGAGCCTCCCTCAGCCACGCTCTCTCAGCCAGGCTCT 1676

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## RESULT 7

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US-09-167-354-5
; Sequence 5, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-5

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## Alignment Scores:

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Pred. No.:      5,72e-65      Length:      2699
Score:          724.50      Matches:      171
Percent Similarity: 48.9%      Conservative: 52
Best Local Similarity: 37.5%      Mismatches: 118
Query Match:      35.4%      Indels:      115

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DB:      3      Gaps:      12
US-10-626-445-8 (1-391) x US-09-167-354-5 (1-2699)
Qy      18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db      407 CTGGCCGGCTCATGGCGCTCTCATCGTGGCCACGGGTGCTGGGCNAGCGCTGGTCATG 466
Qy      38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db      467 CTCGCCCTTCGTGGCGCACTCGAGCTCCGACCCAGAACCAACTTCTCTCTCTCAACCTC 526
Qy      58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db      527 GCCATCTCCGACTTCTCTCGTCGGCGCTTCTGCATCCCACTGTATGATCCCTCATGTCGT 586
Qy      78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db      587 ACAGGCGCTGGACCTTTCGGCCGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTG 646
Qy      97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db      647 CTGTGCACTCTCTCTGCTTCAACATCTGCTCATCAGCTACGACCGCTTCTCTGTGGTCTC 706
Qy      117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db      707 ACCGAGCGGTCTCATACCGGCGCCACAGGTGACACGGCGCGGCGAGTGGCGAAGATG 766
Qy      137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db      767 CTGCTGTGTGGGTGCTGGCTTCTCTCTGTCAGGACCGACCATCTCTG-----AGC 817
Qy      157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db      818 TGGAGTACCTGTCGCGGGGCGAGCTCCATCCCGAGGCGCACTGCTATGCGAGTTCTTC 877
Qy      172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db      878 TACAACCTGGTACTTCTCTCATCAGCGCTTCCACCTGGAGTTCTTTTACGCCCTTCTCTCAGC 937
Qy      192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db      938 GTCACTTCTTTAACTTCACTCAGCATCTACTGAACATCCAGAGGCGCACCCGCGCTCGGGCTG 997
Qy      200 ----- 200
Db      998 GATGGGCTCGAGAGGCGAGCGCGCCCGAGCCCTCCCGAGGCGCCAGCCCTCACACCC 1057
Qy      201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db      1058 CCACCGCTCGCTGTGGGCTGCTGGCAGAGGGGCGACGGGAGGAGGATGCCCTCGTCGAC 1117
Qy      216 -----AlaGlyPheSerThrThrSerSer 223
Db      1118 AGGTATGGGTGGGTGAGCGCGCGTAGGCGCTGAGGCGCGGGAGGCGACCTCGGGGGT 1177
Qy      224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db      1178 GCGCGTGGGGC-----GGCTCGCTGGCTTCAACCCACTCCAGCTCCAGCTCGCGC--- 1222
Qy      244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db      1223 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 1252
Qy      264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db      1253 -----TCACTCAAGAGGGGCTCAAGCCGTCG 1279
Qy      284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db      1280 GCGTCTCGGCTCTCGCTGGAGAGCGCATGAAGATGGTGTCCCAGAGCTTCAACCCAGCGC 1339
Qy      295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaLleLeuLeuSerAlaPhe 314

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Db      1340 TTTTCGGCTGCTCGGACAGAAAGTGGCAAGTCGCTGGCGTCATCGTGAGCATCTTT 1399
Qy      315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db      1400 GGGCTCTGCTGGGCCCATACAGCTCTGATGATCATCCGGCCGCTGCCATATGGCCAC 1459
Qy      335 GluArgProLysSerValTyrTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPhe 354
Db      1460 TGGCTCCCT---GACTACTGGTACGAAACCTCTCTTCTGGCTCTCTGGGCCCACTCGGCT 1516
Qy      355 ValAsnProLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db      1517 GTCAACCTCTGCTCTACCTCTGTGCCACACAGCTTCCGGCGGCTTCCACCAAGCTG 1576
Qy      375 LeuCysValThrLys-----ProAlaLeuSerGlnAsnGlnSer 388
Db      1577 CTCTGCCCCCAGAGACTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGA 1636
Qy      381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db      1637 GTGGCCCCACAGAGCTCCCTCAGCCCAAGCTCTCTCAGCCCCAGGTCT 1684

RESULT 8
US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Javaahree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

Alignment Scores:
Pred. No.: 5,72e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 3 Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-855-5 (1-2699)
Qy      18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db      407 CTGGCCGGCTCATGGCGCTGCTCATCGTGGCCACCGTGTGGGCCAAGCGCTGTGTCATG 466
Qy      38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db      467 CTCGCCCTTCTGGCGCGACTCGAGGCTCCGACCCAGAACAACTTCTTCTCTGCTCAACCTC 526
Qy      58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIle 77
Db      527 GCCATCTCCGACTTCTCTGCTGGCGGCTTGTGCATCCACATGATGATCCCTACGTGCTG 586
Qy      78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96

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Db      587 ACAGGCGCTGGACCTTCGGCCGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACTCTG 646
Qy      97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db      647 CTGTGACACTCTCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTCTGCTGGTCTC 706
Qy      117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db      707 ACCGAGCGGTCTCATACCGGGCCAGCAGGGGTGACACGGCGGGGCGAGTGGCGAAGATG 766
Qy      137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db      767 CTGCTGTGTGGTGTGGCTTCTCTGCTGTACGAGCCAGCCATCTCTG-----AGC 817
Qy      157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db      818 TGGGAGTACCTGTCCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTC 877
Qy      172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db      878 TACAACCTGGTACTTCTCTCATCAGGGCTTCCACCTTGGAGTCTTTTACGCGCTCTCTCAGC 937
Qy      192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db      938 GTCACTTCTTTAACTTCACTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCTCCGGCTG 997
Qy      200 ----- 200
Db      998 GATGGGGCTCGAGAGGAGCGCGCGCCCGAGCCCTCCCGAGGCCAGCGCTCACACACC 1057
Qy      201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db      1058 CCACCGCTCGGCTGCTGGGGCTGCTGGCAGAGGGCAGCGGGAGGCGCATGCGCTCGAC 1117
Qy      216 -----AlaGlyPheSerThrThrSerSer 223
Db      1118 AGGTATGGGGTGGGTGAGGGCGCGCTAGGCGCTCAGGCGCGGGAGGCGCGCTCGGGGT 1177
Qy      224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db      1178 GCGGTGGGGG-----GGCTCGTGGCTTACCCACCTCCAGCTCGGCG--- 1222
Qy      244 LysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSerIleLeuVal 263
Db      1223 -----AGCTCTCGAGGGCGACTGAGAGCGCGGC----- 1252
Qy      264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db      1253 -----TCACTCAAGAGGGGCTCCAAAGCGCTCG 1279
Qy      284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db      1280 GCGTCTCGCGCTCGCTGGAGAGCGCATGAGATGTGTGCCAGAGCTTCACCCAGCGC 1339
Qy      295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db      1340 TTTTCGGCTGTCTCGGACAGGAAAGTGCACAGTGTGCGCTGCTGCGCTCATCGTGCAGCATCTT 1399
Qy      315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db      1400 GGGCTCTGCTGGGCCCATACAGCTCTGATGATCATCCGGCCGCTGCCATGGCCAC 1459
Qy      335 GluArgProLysSerValTyrTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPhe 354
Db      1460 TGGCTCCCT---GACTACTGGTACGAAACCTCTCTTCTGGCTCTCTGGGCCCACTCGGCT 1516
Qy      355 ValAsnProLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db      1517 GTCAACCTCTGCTCTACCTCTGTGCCACACAGCTTCCGGCGGCTTCCACCAAGCTG 1576
Qy      375 LeuCysValThrLys-----Trp----- 380
Db      1577 CTCTGCCCCCAGAGACTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGA 1636

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Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1637 GTGCCCCACAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCAGGTCT 1684

RESULT 9
; Sequence 5, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-5

Alignment Scores:
Pred. No.: 5,72e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 3 Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-514-5 (1-2699)

Qy 18 LeuAlaPheLeuMetSerPheAlaPheAlaMetValGlyAsnAlaValValle 37
Db 407 CTGCGCGGCTCATGGCGTCTCATGTGGCCACGCTGTGGCAACGCTGTGTCATG 466

Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTCGCTTCGTGGCGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTC 526

Qy 58 AlaLeuSerAspPheLeuValGlyLeuLeuSerLeuProLeuTyrLeuProHisValLeu 77
Db 527 GCCATCTCCGACTTCTCTCGTGGCGGCTTGTGCATCCCACTGTATGATACCTAGCTG 586

Qy 78 Phe---AsnTrpAsnPheGlySerGlyLeuCysMetPheTrpLeuLeuThrAspTyrLeu 96
Db 587 ACAGGCGCTGGACCTTCGCGCGGCGGCTCTGCAAGTGTGGTGGTAGTGACTACCTG 646

Qy 97 LeuCysThrAlaSerValTyrAsnLeuValLeuLeuSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGCACTTCCTCTGCTTCAACATGTGCTCATAGTACGACCGCTTCTCTCGGTC 706

Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyLeuMetLysLeuAlaGlnMet 136
Db 707 ACCCGAGCGGTCTCATACCGGGCCAGCAGGGGTGACACGCGCGCGGCGAGTGGCGAAGATG 766

Qy 137 ValAlaValTrpLeuLeuAlaPheLeuValAsnGlyProMetLeuLeuAlaSerAspSer 156
Db 767 CTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 817

Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 818 TGGGAGTACCTGTCCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTC 877
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Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 878 TACAACGGGTACTTCTCTCATCAGCGCTTCCACCGCTGGAGTCTTTTACGCCCTTCTCAGC 937

Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 938 GTCACTTCTTTAACTTCACTCAGCATCTACTGAACATCCAGAGGCGCACCGCTCGGCTG 997

Qy 200 ----- 200
Db 998 GATGGGCTCGAGAGGCGAGCGGCCCGAGCCCTCCCGAGGCCAGCCCTCACCACCC 1057

Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 1058 CCACCGCTGGCTGTGGGCTGTGGCAGAAGGGGCGAGGGAGGCATCCCGCTGCAC 1117

Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1118 AGGTATGGGTGGGTGAGCGCGCTAGCGCTGAGCGCGGGGAGGCGCACCTCTCGGGGT 1177

Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1178 GCGGTGGGCGC-----GGCTCGTGGCTTCAACCACTCCAGCTCGGCGC--- 1222

Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1223 -----AGCTCTCGAGGCGCACTGAGAGCGCGCGC----- 1252

Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 1253 -----TCACTCAAGAGGGGCTTCAAGCGCTCG 1279

Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1280 GCGTCTCGGCTCGCTGAGAGAGCGCATGAAGATGTTGCCAGAGCTTCAACCGCGC 1339

Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaLeuLeuSerAlaPhe 314
Db 1340 TTTCGGCTGTCTCGGACAGGAAGTGGCCGCTGCTGGCGCTCATCGTGAAGATCTTT 1399

Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1400 GGGCTCTGCTGGGCGCCATACACGCTCTGATGATCATCCGGCGCGCTGCGATGGCCAC 1459

Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1460 TGGTCCCT---GACTACTGTGTACGAAACCTCTCTGCTGCTCTGTGGCGCAACTCGGCT 1516

Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1517 GTCAACCTGTCTCTTACCTCTGTGCCACACACAGCTTCCGCGGGGCTTCCACCAAGCTG 1576

Qy 375 LeuCysValThrLys-----Trp----- 380
Db 1577 CTCTGCCCCCAGAGCTCAAAATCCAGCCACAGTCCCTTGGAGACTGCTGGAAGTGA 1636

Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1637 GTGGCCACACAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCAGGTCT 1684

RESULT 10
US-09-642-852-5
; Sequence 5, Application US/09642852
; Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,852
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; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-852-5

Alignment Scores:
Pred. No.: 5,72e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 12 Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-852-5 (1-2699)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle 37
Db 407 CTGGCGCGCTCATGGCGCTCATCGTGGCCACCGGTGTGGCAACGCGTGGTTCATG 466

Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTGGCGCTTCGTGGCGGCTCGGAGCTCCGACCCAGAACAACTTCTTCCTCGCTCAACCTC 526

Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIlePheLeuTyrIleProHisValLeu 77
Db 527 GCCATCTCCAGCTTCCTCGTGGCGGCTCTGCAATCCACTGTATGATGACCTACGTGCTG 586

Qy 78 Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeu 96
Db 587 ACAGGCGCTGGACCTTCGCGCGGCTCTGCAAGCTGTGGTGTAGTGAGTACTCTG 646

Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGCACTCTCTGCTGCTCAACATCGTGTATCATGCTACAGTACGACCGCTTCCTGTG 706

Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMet 136
Db 707 ACCGAGCGGTCTCATACCGGCGCCAGCAGGGTGACACGGCGGCGGAGTGGCGGAAGTG 766

Qy 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 767 CTGCTGGTGTGGTGTCTGGCTTCTCTGTACGACCGACCATCTCTG-----AGC 817

Qy 157 TrpIys-----AsnSerThrAsnThrIysAspCysGluProGlyPheVal 171
Db 818 TGGGAGTACCTGTCTCGGCGGCGAGCTCCATCCCGAGGCGCAGCTGCTATGCGGAGTTCTTC 877

Qy 172 ThrGluTyrIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
Db 878 TACACTGGTACTTCTTCATCAGCGTTCACCCCTGGAGTCTTTACGCGCTCTCTCAGC 937

Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 938 GTCACCTCTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCTCGGCGTG 997

Qy 200 ----- 200
Db 998 GATGGGCTCGAGAGCGCGGCGCCCGAGCCCTCCCGAGGCGCCAGCCCTCACACCC 1057

Qy 201 -----TrpSerLeuTyrIleArgAlaLeuSerArgCysProSerHis 215
Db 1058 CCACCGCTGCTGCTGGCGGTGCTGGCAGAAAGGGGACCGGGAGGCGCATGCGCTGCAC 1117

Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 223 -----AlaGlyPheSerThrThrSerSer 223
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Db 1118 AGGTATGGGTGGTGGTGGCGCGCTAGGCGCTCAGGCGCGGAGGCGAGCCCTCGGGGGT 1177
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1178 GCGCGTGGGGC-----GGCTCGTGGCTTACCCACCTCCAGCTCGGCG----- 1222
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1223 -----AGCTCTCGAGGGGCACTGAGAGCGCGGCG----- 1252
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTyrArg 283
Db 1253 -----TCACTCAAGAGGGGCTCCAAAGCCGCTCG 1279

Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1280 GCGTCTCGCGCTCGCTGGAGAGCGCATGAAGATGTGTCCAGAGCTTACCCAGCGC 1339
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1340 TTTCGGCTGTCTCGGACAGGAAAGTGGCAAGTGGCTGGCGCTCATCGTGAGCATCTTT 1399

Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1400 GGGCTCTGTGGGCGCCCATACAGCTGCTGATGATCATCCGCGCGCGCTGCCATGGCCAC 1459
Qy 335 GluArgProLysSerValTyrTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPhe 354
Db 1460 TGGGTCCCT---GACTACTGTGTACGAACCTCTCTGTGGCTCTCTGTGGGCACTCGGCT 1516

Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1517 GTCAACCTGTCTCTACCTCTGTGCCACACAGCTTCCGCGGCGCTTACCCAGCTG 1576

Qy 375 LeuCysValThrIys-----Trp----- 380
Db 1577 CTCTGCCCCAGAAAGCTCAAAATCCAGCCACAGCTCCCTGGAGCAGCTGCTGGAAGTGA 1636

Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1637 GTGGCCACACAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCCGAGGTCT 1684

RESULT 11
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 742-4214  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1335 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1335  
 US-08-985-090-3

## Alignment Scores:

Pred. No.: 2,89e-65 Length: 1335  
 Score: 722.50 Matches: 165  
 Percent Similarity: 50.8% Conservatives: 51  
 Best Local Similarity: 38.8% Mismatches: 116  
 Query Match: 35.3% Indels: 93  
 DB: 2 Gaps: 10

US-10-626-445-8 (1-391) x US-08-985-090-3 (1-1335)

QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValValle 37  
 DB 109 CTGGCCGCTCATGCGCTGCTCATCGTGGCCACCGGTGCTGGGCAACGCGCTGTCATG 168  
 QY 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  
 DB 169 CTGGCTTCGTGGCGACTCGAGCTCCGACCCAGAACAACTTCTTCGTCTCAACCTC 228  
 QY 58 AlaileSerAspPheLeuValGlyLeuileSerileProLeuTyrileProHisValleu 77  
 DB 229 GCCATCTCCGACTTCCTCGTGGCGCTCTGTCATCCCACTGTATGTACCTAGTGTGCTG 288  
 QY 78 Phe---AsnTrpAsnPheGlySerGlyleCysMetPheTrpLeulleThrAspTyrLeu 96  
 DB 289 ACAGGCGCTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGTGTAGTGGACTACCTG 348  
 QY 97 LeuCysThrAlaSerValTyrAsnileValleuileSerTyrAspArgTyrGlnSerVal 116  
 DB 349 CTGTGACCTTCCTGCTTCAACATGCTGCTATCATGCTACGACCCGCTTCCTGTCGCTC 408  
 QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyleMetTyrileValAlaGlnMet 136  
 DB 409 ACCGAGCGCTCTCATACCGGGCCAGCAGCGGTGACACGCGGGCGAGTGGCGAAGATG 468  
 QY 137 ValAlaValTrpLeuAlaPheLeuValAsnGlyProMetileLeuAlaSerAspSer 156  
 DB 469 CTCTGTGTGGGTGTGGCTTCTCTGCTGTACGGACCACTATCTG-----AGC 519  
 QY 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171  
 DB 520 TGGAGTACCTGTCCGGGGCAGCTTCATCCCGAGGGCCACTGCTATGCGGAGTCTTC 579  
 QY 172 ThrGluTrpTyrileThrMetLeuLeuGluPheLeuProValileSer 191  
 DB 580 TACAACCTGGTACTTCCTCATCAGCGCTTCACCCCTGGAGTCTTTACGCGCTTCCTCAGC 639  
 QY 192 ValAlaTyrPheAsnValGlnileTyr----- 200  
 DB 640 GTCACCTTCTTTAACCTCAGCATCTACCTGAACATCCAGAGGGCGACCCGCTCCGCGCTG 699  
 QY 200 ----- 200  
 DB 700 GATGGGCTCGAGGAGCGCGGCGCGCCCTCCCGAGGCCAGCCCTCACACCC 759  
 QY 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215  
 DB 760 CCACCGCTGGCTGCTGGGCTGCTGGCAGAGGGGACCGGGAGGCGCATGCGCTCCAC 819  
 QY 216 -----AlaGlyPheSerThrThrSerSer 223

DB 820 AGGTATGGGTGGGTGAGCGCGCGTGTAGCGCGTGTAGCGCGGAGCGACCTCGGGGT 879  
 QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243  
 DB 880 GCGCGTGGGGC-----GGCTCGTGGCTTCCACCACCTCCAGCTCCGGC--- 924  
 QY 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerileLeuVal 263  
 DB 925 -----AGTCTCTCAGGGGCACTCAGAGGCGCGC----- 954  
 QY 264 SerLeuArgThrHisMetAsnSerSerileThrAlaPheLysValGlySerPheTrpArg 283  
 DB 955 -----TCACTCAAGAGGGGCTCCAAGCCGTGC 981  
 QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294  
 DB 982 GCGTCTCGCGCTCACTGGAGAGCGCATGAAGATGTGTCCAGAGCTTCCACCACGCGC 1041  
 QY 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaileLeuLeuSerAlaPhe 314  
 DB 1042 TTTGCGCTGTCTCGGGACAGGAAAGTGGCAAGTGTGGCGCTCATCGTGAAGCATCTTT 1101  
 QY 315 AlaileCysTrpAlaProTyrCysLeuPheThrileValLeuSerThrTyrProArgThr 334  
 DB 1102 GGGCTCTGCTGGGCCCCATACGCTGCTGATGATCATCGGGCGCGCTGCCATGGCCAC 1161  
 QY 335 GluArgProLysSerValTrpTyrSerileAlaPheTrpLeuGlnTrpPheAsnSerPhe 354  
 DB 1162 TGGCTCCCT---GACTACTGTAGTACGAAACCTCTTCTGGCTCTCTGGCCAACTCGGT 1218  
 QY 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysile 374  
 DB 1219 GTCAACCTCTCTCTACCTCTGTGCCACACAGCTTCCGCGCGGCTTCCACCAAGCTG 1278  
 QY 375 LeuCysValThrLys 379  
 DB 1279 CTCTGCCCCCAGAG 1293

## RESULT 12

US-09-165-543-3  
 Sequence 3, Application US/09165543  
 Patent No. 6093545  
 GENERAL INFORMATION:  
 APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman  
 TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/165,543  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/042,780  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Elizabeth A. Hanley  
 REGISTRATION NUMBER: 33,505  
 REFERENCE/DOCKET NUMBER: MNI-032CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 742-7400  
 TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1335 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1335

; US-09-165-543-3

Alignment Scores:

Pred. No.: 2,89e-65 Length: 1335

Score: 722.50 Matches: 165

Percent Similarity: 50.8% Conservative: 51

Best Local Similarity: 38.8% Mismatches: 116

Query Match: 35.3% Indels: 93

DB: Gaps: 10

US-10-626-445-8 (1-391) x US-09-165-543-3 (1-1335)

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QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValValle 37
DB 109 CTGGCGCGCTCATGGCGCTGCTCATCGTGCACCGGTGCTGGGCAAGCGGTGTCATG 168
QY 38 LeuAlaPheValValAspArgAsnLeuArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
DB 169 CTGGCGCTTCGTGGCGACTCGAGCTCCGACCCAGAACCACTTCTTCTGCTCAACCTC 228
QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIlePheLeuTyrIleProHisValLeu 77
DB 229 GCCATCTCCGACTTCCTCGTGGCGGCTTCGTGATCCCATCTGATGATGATGATGATGATG 288
QY 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
DB 289 ACAGGCGCTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGTGGTAGTGAGTACCTG 348
QY 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
DB 349 CTGTGCACCTTCCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTGTCGGTCT 408
QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetValGlyValAlaGlnMet 136
DB 409 ACCGAGCGGTCTCATACCGGGCCACAGCGGTGACAGCGGGCGGCGAGTGCAGAGATG 468
QY 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DB 469 CTGCTGTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
QY 157 TrpIys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
DB 520 TGGGAGTACCTGTCGGGGGCGAGCTCCATCCCGAGGCGCAGCTGCTATGCGGAGTCTTC 579
QY 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
DB 580 TACAACCTGGTACTTCTCATCAGCGCTTCACCTCGGAGTCTTTACGCGCTCTCTCAGC 639
QY 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
DB 640 GTCACCTTCTTAACCTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCTCCGGCTG 699
QY 200 ----- 200
DB 700 GATGGGCTCGAGAGGCGCGGCGCGAGCCCTCCCGAGGCGCCAGCCCTCACACCC 759
QY 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
DB 760 CCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
QY 216 -----AlaGlyPheSerThrThrSerSer 223
DB 820 AGGTATGGGTGGTGGAGGCGCGTAGGCGCTGAGGCGCGGGAGGCGACCTCGGGGT 879
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QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
DB 880 GGCGGTGGGGC-----GGCTCGTGGCTTACCCACCTCCAGCTCCGGC--- 924
QY 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSerIleLeuVal 263
DB 925 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 954
QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySerPheTrpArg 283
DB 955 -----TCACTCAAGAGGGGCTCCAAGCCGCTCG 981
QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
DB 982 GCGTCTCGGCTCACTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCACCCAGCGC 1041
QY 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
DB 1042 TTTTCGGCTGTCTCGGGACAGGAAAGTGGCAAGTCTGTCGCGCTCATCGTGGAGCATCTTT 1101
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
DB 1102 GGGCTCTGCTGGGCCCATACACGCTGCTGATCATCGGGCGCGCTGCCATGGCCAC 1161
QY 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
DB 1162 TGGCTCCCT---GACTACTGGTACGAAACCTCTCTTGGCTCTGTGGGCAACTCGGCT 1218
QY 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpIle 374
DB 1219 GTCAACCTGCTCTCTACCTCTGTGCCACACAGCTTCCGCGGGCGCTTCACCAAGCTG 1278
QY 375 LeuCysValThrLys 379
DB 1279 CTCTGCCCCCAGAG 1293
RESULT 13
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-167-354-6
Alignment Scores:
Pred. No.: 2,89e-65 Length: 1335
Score: 722.50 Matches: 165
Percent Similarity: 50.8% Conservative: 51
Best Local Similarity: 38.8% Mismatches: 116
Query Match: 35.3% Indels: 93
DB: Gaps: 10
US-10-626-445-8 (1-391) x US-09-167-354-6 (1-1335)
QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValValle 37
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Db 109 CTGGCCGGCTCATGCGCTGCTCATCGTGCCACCGGTGCTGGCAACGCGCTGGTCATG 168  
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Db 169 CTCGCCCTTCGTGGCGGAGCTCGAGCGTCGCAACCCAGAACAACTCTCTCTGCTCAACCTC 228  
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIlePheLeuValLeu 77  
Db 229 GCCATCTCCGAGCTTCCTGCTGGCGCCTTCGCAATCCCACTGTATGATACCTACGTGCTG 289  
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96  
Db 289 ACAGCCCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTCTG 348  
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116  
Db 349 CTGTGCACCTCTCTGCTGCTCAACATCGTGTCTATCAGTACGACCGCTCTCTGCTGGTC 408  
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136  
Db 409 ACCCGAGCGGTCTCATACCGGGCCGACGAGGGTGACACGCGGGCGAGTGCGGAAGATG 468  
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156  
Db 469 CTGCTGTGTGGGTCTGCTGGCTTCTGCTGTACGACGACGACCTCTG-----AGC 519  
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171  
Db 520 TGGGAGTACCTGTCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCTTC 579  
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191  
Db 580 TACAACCTGGTACTTCTCTCATACGCGTTCACCCCTGGAGTCTTTACGCGCTCTCTCAGC 639  
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200  
Db 640 GTCACTTCTTTAACCCTCAGCATCTACTGNACTCCAGAGGCGCACCCGCTCCGGCTG 699  
Qy 200 ----- 200  
Db 700 GATGGGCTCGAGAGCGAGCGGCGCCGAGCGCCCTCCGAGGCGCCAGCCCTCACACCC 759  
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215  
Db 760 CCACCGCTGCTGCTGCTGGCGCTGTGCGAGAAGGGGACCGGGAGGCCATCGCCGCTCAC 819  
Qy 216 -----AlaGlyPheSerThrThrSerSer 223  
Db 820 AGGTATGGGTGGGTGAGGCGGCGGTAGGCGCTGAGCGCGGGAGGCGACCTCGGGGGT 879  
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243  
Db 880 GCGGTGGGGC-----GGCTCCGTGGCTTCAACCCACTCCAGCTCCGCGC----- 924  
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263  
Db 925 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 954  
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283  
Db 955 -----TCACTCAAGAGGGGCTCAACGCCCTCG 981  
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294  
Db 982 CGCTCTCGGCTCGCTGGAGAGCGCATGAAGATGTGTCCAGAGCTTCACCCAGCGC 1041  
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314  
Db 1042 TTTCCGCTGTCTCGGAGAGAAAGTGGCCAAAGTCGCTGGCGCTCATCGTAGCATCTTT 1101  
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334  
Db 1102 GGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGGCGCGCTGCGATGGCCAC 1161

Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354  
Db 1162 TGCCTCCT---GACTACTGGTACGAACCTCTCTCTGCTCTCTGGGCCAATCTGGCT 1218  
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374  
Db 1219 GTCNACCTCTCTCTTACCTCTGTGTCACCAACAGCTTCGCGCGGGCTTCACCAAGCTG 1278  
Qy 375 LeuCysValThrLys 379  
Db 1279 CTCTGCCCCCAGAAG 1293  
RESULT 14  
US-09-642-855-6  
; Sequence 6, Application US/09642855  
; Patent No. 6413743  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/642,855  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-642-855-6

## Alignment Scores:

Pred. No.: 2,89e-65 Length: 1335  
Score: 722.50 Matches: 165  
Percent Similarity: 50.8% Conservative: 51  
Best Local Similarity: 38.8% Mismatches: 116  
Query Match: 35.3% Indels: 93  
DB: 3 Gaps: 10

US-10-626-445-8 (1-391) x US-09-642-855-6 (1-1335)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37  
Db 109 CTGGCCGCTCATGCGCTGCTCATCGTGCCACCGGTGCTGGCAACGCGCTGGTCATG 168  
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  
Db 169 CTGCGCTTCGTGGCGGACTCGAGCTCCGACCCAGAACAACTCTCTCTGCTCAACCTC 228  
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIlePheLeuTrpLeuIleThrAspTyrLeu 77  
Db 229 GCCATCTCCGAGCTTCCTGCTGGCGCCTTCGATCCCACTGTATGATACCTACGTGCTG 288  
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96  
Db 289 ACAGCCCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTCTG 348  
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116  
Db 349 CTGTGCACCTCTCTGCTGCTTCAACATCGTGTCTATCAGTACGACCGCTCTCTGCTGGTC 408  
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136  
Db 409 ACCCGAGCGGTCTCATACCGGGCCGACGAGGGTGACACGCGGGCGAGTGCGGAAGATG 468

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Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGGTGCTGGCTTCTGCTGTACGGACCGACCTCCTG-----AGC 519
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 520 TGGAGTAGTCTGTCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTC 579
Qy 172 ThrGluTrpTrpIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
Db 580 TACAACCTGGTACTTCTTCATACCGCTTCCACCTCGGAGTTCTTTACGCCCTTCTCCTCAGC 639
Qy 192 ValAlaTrpPheAsnValGlnIleTyr----- 200
Db 640 GTACACCTTCTTTAACCTCAGCATCTACTGNAACATCCAGAGGCCACCGCCCTCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGCTCGAGAGGCGAGCGGCCCGAGCCCTCCCGAGGCCCGCCTCACACCCC 759
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 760 CCACCGCTGGCTGCTGGGGCTGTGTGAGAGAGGGGCGAGGGGAGGCATGCCGCTGCAC 819
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 820 AGGTATGGGTGGGTGAGCGCGCGTAGCGCTGAGCGCGGGGAGGCGACCTCGGGGGT 879
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 880 GCGCGTGGGGC-----GGCTCGGTGCTTCCACCCACTCCAGCTCGGCGC--- 924
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 925 -----AGCTCTCGAGGGGCACTGAGAGGCGCGC----- 954
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
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Db 982 GCGTCTCGGCTCGCTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCACCCAGCGC 1041
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1042 TTTCCGGCTGTCTCGGACAGGAAAGTGGCCAAAGTCGCTGGCCGTCATCGTGAGCATCTTT 1101
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Db 1219 GTCAACCCCTGTCCTTACCTCTACCTCTGTGCCACCACACAGCTTCGCGGGGCTTCACCAAGCTG 1278
Qy 375 LeuCysValThrLys 379
Db 1279 CTCTGCCCCCAGAG 1293
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## RESULT 15

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US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
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; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-6

Alignment Scores:
Pred. No.: 2,89e-65 Length: 1335
Score: 722.50 Matches: 165
Percent Similarity: 50.8% Conservative: 51
Best Local Similarity: 38.8% Mismatches: 116
Query Match: 35.3% Indels: 93
DB: 3 Gaps: 10

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Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTGCGCTTGTGGCGGACTCGAGCTCCGACCCAGAACAACTTCTCTCTCAACCTC 228
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 229 GCCATCTCCGACTTCTCTCGTGGCGCTTCTGCATCCCACTGTATGTACCTACGTCGTG 288
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGGCGCTGGACCTTTCGGCCGGGGCTCTGCAAGCTGTGGCTGGTGGAGTACCTCG 348
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACTCTCTGCTTCAACATGCTGCTCATAGCTACGACCGCTTCTCTCGGTC 408
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 409 ACCCGAGCGGTCTCATACCGGGCCAGAGGGTGCACGCGGGCGGCGGAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGGTGCTGGGCTTCTCTGTGTACGACCGACCATCTCCTG-----AGC 519
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 520 TGGGAGTACCTGTGCGGGGCGAGCTTCTCCCGAGGGCCACTGCTATGCGGAGTTCTTC 579
Qy 172 ThrGluTrpTrpIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
Db 580 TACAACCTGGTACTTCTCTCATCCGCTTCCACCTCGGAGTTCTTTACGCCCTTCTCCTCAGC 639
Qy 192 ValAlaTrpPheAsnValGlnIleTyr----- 200
Db 640 GTACACCTTCTTTAACCTCAGCATCTACTGAAATCCAGAGGCCACCGCCCTCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGCTCGAGAGGCGAGCGGCCCGAGCCCTCCCGAGGCCCGCCTCACACCCC 759
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
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Db 760 CCACCGCTGGCTGCTGGGGCTGCTGGCAGAGGGGCACGGGAGGCCATGCCGCTGCAC 819
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 820 AGGTATGGGTGGGTGAGCGCGCCGTAGCGCGTGGGCGCGGAGGCCACCTCGGGGGT 879
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 880 GCGGTGGGGC-----GGCTCCGTGGCTTCAACCCACCTCCAGCTCCGCGC--- 924
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Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 955 -----TCACCTCAAGAGGGCTCCAAGCCGTCG 981
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 982 GCGTCTCGGCTCGCTGGAGAAGCGCATGAAGATGGTGTCCAGAGCTTCAACCCAGCGC 1041
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1042 TTTCGGCTGTCTCGGGACAGGAAGTGGCCAAAGTCGCTGGCGGTCACTCGTGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1102 GGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGGCGCGCTGCATGGCCAC 1161
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Db 1162 TGGTCCCT---GACTACTGTAGAAACCTCTCTGGCTTCTGTGGGCCAACTCGGCT 1218
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Maximum Match 100%  
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES				
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2	2035	99.4	1176	10 US-10-626-126-5	Sequence 5, Appli
3	2035	99.4	1176	10 US-10-626-398-5	Sequence 5, Appli
4	1745	85.2	1176	9 US-10-626-445-6	Sequence 6, Appli
5	1745	85.2	1176	10 US-10-626-126-6	Sequence 6, Appli
6	1745	85.2	1176	10 US-10-626-398-6	Sequence 6, Appli
7	1370.5	66.9	1170	10 US-10-488-421-7	Sequence 7, Appli
8	1370.5	66.9	1173	3 US-09-812-216-1	Sequence 1, Appli
9	1370.5	66.9	1173	3 US-09-910-411-1	Sequence 1, Appli
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11	1370.5	66.9	1173	3 US-09-876-252-13	Sequence 13, Appli
12	1370.5	66.9	1173	6 US-10-052-193-1	Sequence 13, Appli
13	1370.5	66.9	1173	7 US-10-272-983-13	Sequence 13, Appli
14	1370.5	66.9	1173	7 US-10-354-769-1	Sequence 1, Appli
15	1370.5	66.9	1173	7 US-10-391-807-13	Sequence 13, Appli
16	1370.5	66.9	1173	7 US-10-417-820A-13	Sequence 13, Appli
17	1370.5	66.9	1173	8 US-10-349-253A-1	Sequence 1, Appli
18	1370.5	66.9	1173	8 US-10-723-955-13	Sequence 13, Appli
19	1370.5	66.9	1173	8 US-10-782-596-13	Sequence 13, Appli
20	1370.5	66.9	1173	8 US-10-737-619-1	Sequence 1, Appli
21	1370.5	66.9	1173	9 US-10-626-445-1	Sequence 1, Appli
22	1370.5	66.9	1173	10 US-10-616-088-1	Sequence 1, Appli
23	1370.5	66.9	1173	10 US-10-626-126-1	Sequence 1, Appli
24	1370.5	66.9	1173	10 US-10-626-398-1	Sequence 1, Appli
25	1370.5	66.9	1173	10 US-10-723-955-13	Sequence 13, Appli
26	1370.5	66.9	1266	3 US-09-891-138A-5	Sequence 5, Appli
27	1370.5	66.9	1300	3 US-09-852-165-1	Sequence 1, Appli
28	1370.5	66.9	1300	8 US-10-696-673-1	Sequence 1, Appli
29	1370.5	66.9	3689	6 US-10-225-567A-628	Sequence 628, App
30	1370.5	66.9	3689	9 US-10-684-206-19	Sequence 19, Appli
31	1370.5	66.9	3689	10 US-10-756-149-32	Sequence 32, Appli
32	1366.5	66.7	1173	7 US-10-290-078-26	Sequence 26, Appli
33	1366.5	66.7	1265	7 US-10-230-078-25	Sequence 25, Appli
34	1366.5	66.7	1265	10 US-10-488-421-5	Sequence 5, Appli
35	1238	60.4	1170	9 US-10-626-445-7	Sequence 7, Appli
36	1238	60.4	1170	10 US-10-626-126-7	Sequence 7, Appli
37	1238	60.4	1170	10 US-10-626-398-7	Sequence 7, Appli
38	1198	58.5	1166	10 US-10-488-421-3	Sequence 3, Appli
39	1074.5	52.5	1103	10 US-10-488-421-1	Sequence 7, Appli
40	731.5	35.7	1311	10 US-10-495-679A-7	Sequence 7, Appli
41	724.5	35.4	2689	3 US-09-350-206-1	Sequence 1, Appli
42	724.5	35.4	2689	3 US-09-349-755-1	Sequence 1, Appli
43	724.5	35.4	2689	3 US-09-166-33A-1	Sequence 1, Appli
44	724.5	35.4	2689	6 US-10-282-958-1	Sequence 1, Appli
45	724.5	35.4	2689	13 US-11-059-105-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-10-626-445-5  
; Sequence 5, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent In version 3.2  
; SEQ ID NO 5  
; LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-626-445-5

Alignment Scores: 1.91e-214 Length: 1176  
Pred. No.: 1

Score: 2035.00 Matches: 390  
Percent Similarity: 99.7% Conservative: 0  
Best Local Similarity: 99.7% Mismatches: 1  
Query Match: 99.4% Indels: 0  
DB: 9 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-445-5 (1-1176)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20  
Db 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCACAGCTGCTCAGGTCCCTTGGCATTT 60

Qy 21 LeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValValIleLeuAlaPhe 40  
Db 61 TTAATGCTTCAATTTGGCTTTTGTATTAATGGTGAATGCTGGTCACTTTAGCCCTT 120

Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGGTGACAGAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180

Qy 61 AspPheLeuValGlyLeuIleSerIlePheProLeuTyrIleProHisValLeuPheAsnTyr 80  
Db 181 GACTTCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGGTGTTTAACTGG 240

Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
Db 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTATTACTGACTATCTTTTCTTAATTTGGCTATTCT 300

Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 301 TCTGTCTACAAATATGTCTCTCATTTAGTACATCGATACCATTCAGTTTCAAATGCTGTG 360

Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMetValAlaValTyr 140  
Db 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTGCTCAATGGTGGCTGTGTGG 420

Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160  
Db 421 ATACTGGCTTTCTTGGTAAATGGCCCATGATGATTTGGCTTTCAGATTCTTTGGAAGAACAGC 480

Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180  
Db 481 ACGAACACAAAGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCCACCATTTACA 540

Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 541 ATGCTCTTGGAAATTCCTGCTTCTCTCATCTCTGTGGCTTATTTCAATGTACAGATTTC 600

Qy 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
Db 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGGCCCTAGCCATGCTGGATTCTCCACT 660

Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
Db 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720

Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260  
Db 721 CCTGGATTGAAGGAATCAGCTGTCATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780

Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280  
Db 781 ATCTGGTGTCTTAAAGACTTCATGAAACAGCAGTATCACTGCTTCAAAAGTGGGTTC 840

Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
Db 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGGAGTAGCAGAGCTTCTCAGAGGC 900

Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320  
Db 901 AGGAAGCTAGCAGGTCTACCTGGCCATCTCTGTAGCGCTTTTGTGCAATTTGTGGGCTCCA 960

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340

Db 961 TACTGTCTGTTCAATTTGCTCTTTCAACTTATCCCGAAGCGCCCAAAATCGGTG 1020

Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360

Db 1021 TGGTACAGCATTCCTTCTGGCTGCAATGGTTCAATTCGTTTGAATCCCTTTCTGTATC 1080

Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTyr 380

Db 1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140

Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391

Db 1141 CCAGCGCTGTGCACAGAACCAAGTCAGTATCTTCT 1173

RESULT 2

US-10-626-126-5

; Sequence 5, Application US/10626126

; Publication No. US20050074770A1

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Liu, Changlu

; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype

; FILE REFERENCE: PRD-0033

; CURRENT APPLICATION NUMBER: US/10/626,126

; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849

; PRIOR FILING DATE: 2001-02-22

; PRIOR APPLICATION NUMBER: 60/208,260

; PRIOR FILING DATE: 2000-05-31

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5

; LENGTH: 1176

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-626-126-5

Alignment Scores:

Pred. No.: 1,91e-214 Length: 1176

Score: 2035.00 Matches: 390

Percent Similarity: 99.7% Conservative: 0

Best Local Similarity: 99.7% Mismatches: 1

Query Match: 99.4% Indels: 0

DB: 10 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-126-5 (1-1176)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20  
Db 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCACAGCTGCTCAGGTCCCTTGGCATTT 60

Qy 21 LeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValValIleLeuAlaPhe 40  
Db 61 TTAATGCTTCAATTTGGCTTTTGTATTAATGGTGAATGCTGGTCACTTTAGCCCTT 120

Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGGTGACAGAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180

Qy 61 AspPheLeuValGlyLeuIleSerIlePheProLeuTyrIleProHisValLeuPheAsnTyr 80  
Db 181 GACTTCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGGTGTTTAACTGG 240

Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
Db 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTATTACTGACTATCTTTTCTTAATTTGGCTATTCT 300

Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 301 TCTGTCTACAAATATGTCTCTCATTTAGTACATCGATACCATTCAGTTTCAAATGCTGTG 360

Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMetValAlaValTyr 140

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Db 361 TCTTATAGGGCTCAACACCTGGCATCATGAAGATTGTGCTCAAAATGGTGGCTGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTCCTGGCTTCAGATTCTTGGAGAACAGC 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db 481 ACGAACACAAAGGACTGTGAGCCCTGGCTTGTATACAGAGTGGTACATCCTCACCATTACA 540
Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 541 ATGCTCTTGGATTCCTGCTTCCTGTCATCTCTGGCTTATTTCAATGTACAGATTTC 600
Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGGCCCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
Qy 241 ProGlyLeuLysGluSerAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACAGAAAGTCTCTGGAAGAAAGAGCAGC 780
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 781 ATCTGCTGTCTTTAAGGACTCACATGAACAGCAGTATCACTGCTCTTCAAAGTGGGTTCC 840
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 841 TTCTGGCGCATCGGAAGTGCAGCGCTTCGCCAAAGGGAGTACGACAGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGGTCACTGGCCATCTCTTGAGCGCTTTTGCCATTGCTGGGCTCCA 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 961 TACTGTCTGTTCACAAATGTCTTCACTTACCCAGAGCGGAACGCCCAATCGGTG 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1081 CCATTGTGTACAGCGCTTTCAGAGAGCTTTCGGAAGATACTTTGTGTGACAAAGCAA 1140
Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 1141 CCAGCGCTGTGCAGAACCACTGATCATCTCT 1173
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## RESULT 3

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US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
```

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; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5
Alignment Scores:
Pred. No.: 1,91e-214 Length: 1176
Score: 2035.00 Matches: 390
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.4% Indels: 0
DB: 10 Gaps: 0
US-10-626-445-8 (1-391) x US-10-626-398-5 (1-1176)
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGCGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCAATT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGTCTTCTTATTTGGCTTTGCTATTAATGGTAGGCAATGCTGTGTCATCTTAGCCTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTCTGGGTTTGATTTCATCTCTGTACATCCCTCAGGTGTTGTTAACTGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAAAGTGGAAATCTGCATGTTTTTGGCTCAATTACTGACTATCTTTGTGCACCGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGCTACAAATATGTCTCATTAGCTACGATCAGTACCAGTCAGTTTCAATTTGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTATATAGGCTCAACACACTGGCATCATGAAGATTGTGCTCAATTTGGTGGCTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTCCTGGCTTCAGATTCTTGGAGAACAGC 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db 481 ACGAACACAAAGGACTGTGAGCTTGGCTTTGTGTACAGAGTGGTACATCCTCACCATTACA 540
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTC 600
Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGGCCCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
Qy 241 ProGlyLeuLysGluSerAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 721 CCTGGATTGAAGGAATCAGCTGCATCTCTGTCATCTCAGAAAGTCTCTGGAAGAAAGAGCAGC 780
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 781 ATCTGCTGTCTTTAAGGACTCACATGAACAGCAGTATCACTGCTCTTCAAAGTGGGTTCC 840
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
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Db 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAGGAGTACGACAGCTTCTCAGAGGC 900  
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 901 AGGAAGTACGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTGCTGGGCTCCA 960  
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
Db 961 TACTGCTGTTCAAAATGCTTCACTTACCCAGAGCGGAACGCCCCNAATCGGTG 1020  
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
Db 1021 TGGTACAGCATTCGCTTCGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080  
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380  
Db 1081 CCTTTGTTGTCACAGCGCTTTCCAGAGCGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140  
Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391  
Db 1141 CCAGCGCTGTACAGAACCAAGTCAAGTATCTTCT 1173

## RESULT 4

US-10-626-445-6  
; Sequence 6, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: Rattus rattus  
US-10-626-445-6

## Alignment Scores:

Pred. No.: 2,73e-182 Length: 1176  
Score: 1745.00 Matches: 332  
Percent Similarity: 89.3% Conservative: 17  
Best Local Similarity: 84.9% Mismatches: 42  
Query Match: 85.2% Indels: 0  
DB: 9 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-445-6 (1-1176)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaIleGlnValProLeuAlaPhe 20  
Db 1 ATGTCGGAGTCTAAACGGCACTGACGCTTGTCCACTGTGCTCAAGTCCCTTGGCATTT 60  
Qy 21 LeuMetSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
Db 61 TTAATGTCCTGCTGCTTTGTGTATACGATAGCAATGCTGTGGTCAATTTAGCCCTTT 120  
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80  
Db 181 GACTTCTTCGGGTGTCATCTCCATCTCTGTACATCCCTCACAGCTGTTTAACITGG 240  
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100

Db 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTACTCACTATCTTTTGTGTGCACAGCA 300  
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 301 TCGTCTACAGTATTTGCTTCATTTAGCTACGATCGATACACGTCAGTTTCAAGCGCTGTG 360  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140  
Db 361 CGTTATAGACACAGCACACTGGCATCTCGAAATGTTGCTCAAAATGGTGGCTGTTTGG 420  
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160  
Db 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGAATTCCTTGGAGAAGCAGC 480  
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180  
Db 481 ACCAACACAGAGGAGTGGAGCTTGGCTTTGTTACTGAGTGGTACATCTTCGCCATTACA 540  
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 541 GCATTCTTGGAAATTCCTGCTCCCTGCTCTGTTGGTGTCTATTTTCAGTGTACAGATTAC 600  
Qy 201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
Db 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCTATCGCT 660  
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
Db 661 ACCTCTTCCAGGGCACTGGACACTCAGCAGAACTGGGTGGCTTGTAGGACAAAGTCTT 720  
Qy 241 ProGlyLeuLysGluSerAlaLeuSerArgHisSerGluSerProArgLysSerSer 260  
Db 721 CCTGGATTAAAGGAACCCAGCGCATCTCTTCATTTCAGAAAGTCCACGAGGAAGAGCAGT 780  
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280  
Db 781 CTCCTGGTGTCTTAAGGACTCATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840  
Qy 281 PheTrpArgSerGluSerAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
Db 841 TTCTGCCGATCAGAAAGCCAGTGTCTTCCACAGAGAGACGCTGGAGCTTCTCAGAGGC 900  
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 901 AGGAAGTACGCCAGGTGCTGCTCTGAGTGTCTTTGCAATTTGCTGGGCTCCG 960  
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
Db 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGATT 1020  
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCATTTCAATTCATTATTAATCCCTTCTATAC 1080  
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380  
Db 1081 CCTTTGTCACAGACGCTTTCCAGAGCGCTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140  
Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391  
Db 1141 CCAGCGCTTCCAGACGCCAGTCAAGTATCTTCT 1173

## RESULT 5

US-10-626-126-6  
; Sequence 6, Application US/10626126  
; Publication No. US20050074770A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0033  
; CURRENT APPLICATION NUMBER: US/10/626,126  
; CURRENT FILING DATE: 2003-07-23



; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: Rattus rattus  
US-10-626-126-6

Alignment Scores:  
Pred. No.: 2,73e-182 Length: 1176  
Score: 1745.00 Matches: 332  
Percent Similarity: 89.3% Conservative: 17  
Best Local Similarity: 84.9% Mismatches: 42  
Query Match: 85.2% Indels: 0  
DB: 10 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-126-6 (1-1176)

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Qy 1 MetSerGluSerAenSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAAAGGCACTGAGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATT 60
Qy 21 LeuMetSerPheAlaPheAlaIleMetValGlyAenAlaValValIleLeuAlaPhe 40
Db 61 TTAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGGTGCATTTTAGCCTTT 120
Qy 41 ValValAspArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenLeuAlaIleSer 60
Db 121 GTAGCAGACAGAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCTT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTCTGGGTGTCATCTCCATCTCTGTACATCTCCCTACAGCTGTTTAACTGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTAATGACTATCTTTTGTGCACGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaVal 120
Db 301 TCCGCTACAGTATTGTCTCATTAGCTACGATCGATACAGTCAGTTCATCAAGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 CGTTATAGACACAGCACATGGCATCTGNAATTTGTTGCTCAATGGTGGCTGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCGGCTTCGGATTCTTGGAGAACAGC 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTrpIleLeuThrIleThr 180
Db 481 ACCAACACAGAGGAGTGGAGCTTGTATCTGAGTGGTACATCTCCGCAATACCA 540
Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAenValGlnIleTyr 200
Db 541 GCATCTTGGAAATTCCTGCTCCCTGCTCTCTCTGGTGGTCTATTTCAGTGTACAGATTTC 600
Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 601 TGGAGCTGTGGAGCGTGGAGTCTCAGTAGGTGGCTTAGCCACGCTGGATTTCATCGCT 660
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTGGTCTGTAGCAACAAGTCTT 720
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 721 CCTGGATTAAAGGAACCCAGCGCATCTCCCTCATTTTCAGAAAGTCCACGAGGAAGAGCAGT 780
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Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 781 CTCTCTGGTGTCTTAAAGGACTCATGAGCGGTAGTATCATCGCCTTCAAGTGGGTTC 840
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 841 TTTTGGCGATCAGAAAGCCAGTCTTCCACGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGGTGCTGCTCTGCTGAGTCTTTTGGCAATTTGCTGGCTCCG 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 961 TATTGGCTGTTCACATTTGTTTCAACTTATTCGACAGAGGGAGCGCCCAAAATCGATT 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCATTTCAATTCATTATATCCCTTCTATAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1081 CCTTTGTGTCACAGACGTTTCCAGAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA 1140
Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 1141 CCAGCACCTTCCAGACCCAGTCAGTATCTTCT 1173
RESULT 6
US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6
Alignment Scores:
Pred. No.: 2,73e-182 Length: 1176
Score: 1745.00 Matches: 332
Percent Similarity: 89.3% Conservative: 17
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Query Match: 85.2% Indels: 0
DB: 10 Gaps: 0
US-10-626-445-8 (1-391) x US-10-626-398-6 (1-1176)
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Qy 1 MetSerGluSerAenSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAAAGGCACTGAGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATT 60
Qy 21 LeuMetSerPheAlaPheAlaIleMetValGlyAenAlaValValIleLeuAlaPhe 40
Db 61 TTAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGGTGCATTTTAGCCTTT 120
Qy 41 ValValAspArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenLeuAlaIleSer 60
Db 121 GTAGCAGACAGAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCTT 180
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QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
DB 181 GACTTCTTCGTGGTGATCTCATCTCCCTGTGATCATCTCCACAGCTGTGTTAACTGG 240
QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 AATTTGGAGTGGAACTCGATGTTTGGCTCAATTAAGTACATCTTTTGTGCACAGCA 300
QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCGGCTACAGTATTGTCTCAATAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140
DB 361 CGTTATAGACACAGCACATCGGCATCTGAAATTTGTTGCTCAATAGGTGGCTGTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGATCTTGGGAAGAACAGC 480
QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
DB 481 ACCAACACAGAGAGTGCAGCTGGCTGTGTTACTGAGTGGTACATCTCGCCATTACA 540
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
DB 541 GCATCTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTATATTCAGGTACAGATTTC 600
QY 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 601 TGGAGCTGTGGAGCTGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCAATCGCT 660
QY 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
DB 661 ACCTCTTCCAGGGCACATGGACATCCAGCAGAACTGGTGGCTGTAGGACAAAGTCTT 720
QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSer 260
DB 721 CCTGGATTAAGGAACCCAGCCGATCCCTCATTCAGAAAGTCCAGGAAAGAGCAGT 780
QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
DB 781 CTCCTGTGTCCTTAAGACTCATCATGAGCGGTAGTATCATCGCTTCAAAGTGGTTC 840
QY 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
DB 841 TTCTGCCGATCAGAAAGCCAGTCTTCCAGCAGAGACGACGCTGGAGCTTCTCAGAGGC 900
QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTyrAlaPro 320
DB 901 AGGAAGCTAGCCAGTCCGCTGCTCTCTGAGTCTTTCATTTGCTGGGCTCCG 960
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
DB 961 TATTGCTGTTCACAATGTCTTTCACATATATCGAGAGGGAGCGCCCAATCGATT 1020
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
DB 1021 TGGTACAGCATAGCTTTCGCTACAGTGGTTCATTTCACTTATTAATCCCTTCTATAC 1080
QY 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
DB 1081 CCCTTGTGCACACAGCTTTCAGAGGCTTTCGGAAGACTTCTGTGTGACAAAGCAA 1140
QY 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
DB 1141 CCAGCACTTCACAGACCAGTCAGTATCTTCT 1173
RESULT 7
US-10-488-421-7
; Sequence 7, Application US/10488421
; Publication No. US20050239065A1
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GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc. [US/US]  
; APPLICANT: Gallagher, Michael J.  
; APPLICANT: Yates, Stephen L.  
; TITLE OF INVENTION: HISTAMINE RECEPTOR H4 POLYNUCLEOTIDES  
; FILE REFERENCE: 1367-13335W001  
; CURRENT APPLICATION NUMBER: US/10/488,421  
; CURRENT FILING DATE: 2004-03-01  
; PRIOR APPLICATION NUMBER: US 60/316,762  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/332,697  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1170)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: H4SEQMORSE - Genbank Accession No. AF329449  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066 (2001); U.S. Patent  
; OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Liu - Genbank Accession No. AF312230 - Liu et al., Mol.  
; OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414 A1  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a. sequen  
; OTHER INFORMATION: are AAG and 988 is C  
US-10-488-421-7

Alignment Scores:  
Pred. No.: 9,02e-141 Length: 1170  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.3% Conservative: 40  
Best Local Similarity: 68.1% Mismatches: 82  
Query Match: 66.9% Indels: 3  
DB: 10 Gaps: 2

US-10-626-445-8 (1-391) x US-10-488-421-7 (1-1170)

QY 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20  
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QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40  
DB 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGAAATGCTTTGGTCAATTTAGCTTTT 120  
QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
DB 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCT 180  
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
DB 181 GACTTCTTCGTGGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTGTCGAATGG 240  
QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100

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Db 241 GATTTTGAAGGAAGAACTGGTATTTTGGCTCACTACTGCTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATGATACCTGTCAGTCTCAAAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyLeuMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTTATAGAAGTCAACATCTAGGCTGCTGAAGATTTGTACTCTGATGGTGGCGGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTAGTTTCAGAGTCTTGGAGAGTAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180
Db 481 GGTAAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATCATCTTGGCCATCACA 534
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTGATCCCATCTTAGTCGCTTATTTTCAACATGAATATTAT 594
Qy 201 TrpSerLeuTyrLysAspCysAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCTGTGGAAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCTCGGACTGACTGCT 654
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAACATCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCCTGCTCATCTTTCATTTCAGAGACAGACAGAGAGAGTAGT 774
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTCATGTTTTCCTCAAGAACCAAGATAGCAATAGCAATCAATTTGCTTCCAAATGGGTTC 834
Qy 281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTCTGATGCTCTTCCAAAGGGAACATGTTGAAGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTCTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 955 TATTTCTGTTCACAATTTGCTTTCATTTTATTTCTCAGCAACAGGTCCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGAATTCGATTTTGGCTTCAGTGGTTCATTTCTTTGTCATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgPheGlnLysAlaPheThrLysIleLeuCysValThrLysTyr 380
Db 1075 CCATTGTGTCAAGCGCTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln-----AsnGlnSerValSerSer 391
Db 1135 CCTCTACCATCACAAACAGTCGGTGTAGTATCTTCT 1170
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RESULT 8
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.

```

; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Alignment Scores:
Pred. No.: 9,05e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2

US-10-626-445-8 (1-391) x US-09-812-216-1 (1-1173)
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGCAGATATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTGCTTAGTAGCTTTTGTATATATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTATATTTTTTCTTAATCTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTTGGGTGTGATCTCCATCTCTTTGTATACCTCCCTCACAGCTGTTCCGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTyrIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATGATACCTGTCAGTCTCAAAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAAGTCAACATCTAGGCTTTCGGAATGCTTACTCTGATGGTGGCGGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTCTTTCAGAGTCTTGGAGAGTAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180
Db 481 GGTAAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATCATCTTGGCCATCACA 534
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTGATCCCATCTTAGTCGCTTATTTTCAACATGAATATTAT 594
Qy 201 TrpSerLeuTyrLysAspArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCTGTGGAAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCTCGGACTGACTGCT 654
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAACATCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714

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Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391  
Db 1135 CCTTACCATCACACACAGTCAGTGGTATCTTCT 1170

RESULT 10  
US-09-875-076-13  
; Sequence 13, Application US/09875076  
; Publication No. US20030017528A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-875-076-13

Alignment Scores:  
Pred. No.: 9.05e-141 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.3% Conservative: 40  
Best Local Similarity: 68.1% Mismatches: 82

Query Match: 56.9% Indels: 3  
DB: 3 Gaps: 2  
US-10-626-445-8 (1-391) x US-09-875-076-13 (1-1173)

Qy 1 MetSerGluSerAenSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20  
Db 1 ATGCCAGATACATAATAGCACAAATCAATTTATCACTAGCACTCGTGTACTTTAGCATTT 60  
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAenAlaValValIleLeuAlaPhe 40  
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTAGCTTTT 120  
Qy 41 ValValAspArgAenLeuArgHisArgSerAenTyrPhePheLeuAenLeuAlaIleSer 60  
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCT 180  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAenTyr 80  
Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTGAAATGG 240  
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTACTACTGACTATCTGTTATGTACACA 300  
Qy 101 SerValTyrAenIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaVal 120  
Db 301 TCTGTATATAACATTTGCTCCTCATCAGCTATGATACCTGTGCTGCTCAAAATGCTGTG 360  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValIleValAlaGlnMetValAlaValTyr 140  
Db 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTTGTTACTCTGTGGTGGCGCTTTGG 420  
Qy 141 IleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAspSerTrpLysAenSer 160  
Db 421 GTGCTGGCCTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAA 480  
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180  
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534  
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAenValGlnIleTyr 200  
Db 535 TCATTTCTGGAAATTCGGATCCCGCATCTTAGTCGCTTATTTTCAACATGAATATTAT 594  
Qy 201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
Db 595 TGGAGCCTGTGGAAAGCTGATCATCTCAGTAGGTGCCAAAGCCATCTGGAGTACTGCT 654  
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAen 240  
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714  
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260  
Db 715 TCTGCATCGACAGAAGTTCTCTGTCATCTTCAATTCAGAGACAGAGAGAGAGTAGT 774  
Qy 261 IleLeuValSerLeuArgThrHisMetAenSerSerIleThrAlaPheLysValGlySer 280  
Db 775 CTCATGTTTTCTCAAGAACCAAGATGATAGCAATACAAATGCTTCCAAAATGGTTC 834  
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
Db 835 TTCTCCCAATCAGATTCTGTAGTCTTTCACCAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 895 AGGAGATTACCAAGTCACTGGCCATTTCTTAGGGGTTTTTGTGCTTTGCTGGGCTCCA 954  
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
Db 955 TATTCCTGTTCACAATTTGCTTTCATTTTATTTATTCCTCAGCAACAGGTCCTTAATCAGTT 1014

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Qy 361 ProLeuCysHisArgA-gPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTCAACAGCGCTTTCAAAGCGCTTCTTGAAATATTTTGTATATAAAAGCAA 1134

Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTTACCATCAACAACAGTCGGTCAGTATCTTCT 1170

RESULT 11
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
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; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
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; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-876-252-13

Alignment Scores:
Pred. No.: 9,05e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 3 Gaps: 2

US-10-626-445-8 (1-391) x US-09-876-252-13 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATCTAATAGCAACAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATGCTAGAAATGCTTTGGTCATTTTAGCTTTT 120

Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGCACAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCT 180

Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTTGTGGTGTGATCTCCATTCCTTTGTACATCCCTCACGCTGTTCGAATGG 240

Qy 81 AsnPheGlySerGlyIleCysMetPheTrpIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTATTTTGGCTCACTACTGACTATCTGTATGTATGACACA 300

Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATGATACCTGTCAGTCTCAAAATGCTGTG 360

Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACCTGGGGTCTGGAAGATTGTTACTCTGATGGTGGCGGTTGG 420

Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGAAGATGAA 480

Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db 481 GGATG-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTCCCATCACA 534

Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTGATCCCACTCATCTTAGTCGCTTATTTCAACATGAATATTAT 594
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; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

Alignment Scores:
Pred. No.:          9,05e-141      Length:      1173
Score:             1370.50         Matches:     267
Percent Similarity: 78.3%          Conservative: 40
Best Local Similarity: 68.1%        Mismatches:  82
Query Match:       66.9%           Indels:      3
DB:                7              Gaps:         2

US-10-626-445-8 (1-391) x US-10-354-769-1 (1-1173)

Qy   1 MetSerGluSerAsnThrGlyLeuProAlaGlnValProLeuAlaPhe 20
Db   1 ATGCCAGTACTAATAGACAAATCAATTTATCATAAGCCTCGTGTATTAGCAATT 60
Qy   21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db   61 TTTATGTCCTTAGTAGCTTTTGTCTATATGCTAGGAATGCTTTGGTCATTTTAGCTTTT 120
Qy   41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db   121 GTGGTGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGGCCATCTCT 180
Qy   61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db   181 GACTTCTTTGGGTGTGATCTTCATTTCTTTGTACATCCCTCACGCTGTTCGAATGG 240
Qy   81 AsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db   241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCCTACTACTGCTATCTGTATGTACAGCA 300
Qy   101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db   301 TCTGTATATAACATTTGCTCATCAGCTATGATCGATACCTGTGCTCAGTCTCAAAATGCTGTG 360
Qy   121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140
Db   361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTGTACTCTGTGTTGGGCGCTTTGG 420
Qy   141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160
Db   421 GTGCTGGCCCTTCTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATCAA 480
Qy   161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
Db   481 GGATG-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy   181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db   535 TCATTTCTGGAAATTCGGTATCCCACTCATCTTAGTCGCTTATTTTCAACATGAATATTAT 594
Qy   201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db   595 TGGAGCCTTGGAAACCGTGTATCTCTCAGTAGGTGCGCAAGGCCATCTCGACTGCTCT 654
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Qy   221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db   655 GTCTCTTTCCAAACATCTCTGGCACATCTTCCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy   241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db   715 TCTGCATCGACAGAAAGTTCTCTGCATCTTTCATTTCAGAGACACAGAGGAGAGAGTAGT 774
Qy   261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db   775 CTCATGTTTCTCTCAAGAACCAAGATGAATAGCAATACAATTGCTTCCAAATGGGTTCC 834
Qy   281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db   835 TTCTCCCAATCAGATTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTCTTAGAGCC 894
Qy   301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
Db   895 AGGAGATTAGCCCAAGTCACTGGCCATTTCTTAGGGGTTTTTGTGTTTGGCTGCCCTCA 954
Qy   321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
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Qy   341 TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
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Qy   361 ProLeuCysHisArgArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyr 380
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RESULT 15
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; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liao, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
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; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-13

Alignment Scores:
Pred. No.: 9.05e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 7 Gaps: 2

US-10-626-445-8 (1-391) x US-10-393-807-13 (1-1173)
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAAGCACAATCAATTTATACATAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATATGCTAGGAATGCTTTGGTCATTTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAACCTTAGACATCGAAGTAGTATATTTTCTTAACCTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTTGTGGGTGTGATCTCCATCTCCTTTGTACATCCCTCACACGCTGTTCGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGGAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTTGCTCATCATGATATGATACCTGTGATCTCAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATCTACCTGGGGTCTGAAGATTGTTACTCTGTGCTGGCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLeuAsnSer 160
Db 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGAATCTAGTTTCAGAGTCTTGAAGGATGAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAAATGGTACATCTTGCCATCACA 534
Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATTCGTGATCCCATCTCTTAGTCGCTTATTTTCAACATGAATATTTAT 594
Qy 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGGCCAAAGCCATCTGGACTGACTGCT 654
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCACATCTCTGGGACATCTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluSerAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 715 TCTGCATCGACAGAAGTTCTCTGTCATCTCTTTCATTCAGAGACAGAGAGAGAGAGTAGT 774
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCCTCAAGAACCAAGATGAATAGCAATCAATGCTTCCAAATGGGTCC 834
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Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
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Db 895 AGGAGATTAGCCAAGTCACCTGGCCATTTCTTTAGGGGTTTTTGTCTGTTTCTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 955 TATTCCTGTTCACAATTTGTCCTTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
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Db 1015 TGGTATAGAATTGCAATTTTGGCTTCAGTGGTTCAAATTCCTTTGTCAATCCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTACAAAGCGCTTTCAAAAGGCTTTCTTGAAATATATTTTGTATATAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 25, 2006, 14:08:39 ; Search time 56 Seconds  
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Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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Database : Published Applications NA.New:

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:
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- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1366.5	66.7	1265	7	US-11-242-505A-25
3	297.5	14.5	1847	6	US-10-511-937-2881
4	296	14.5	1323	7	US-11-302-678-42
5	295	14.5	1984	7	US-11-302-678-40
6	295.5	14.4	1074	7	US-11-302-678-39
7	295.5	14.4	1159	7	US-11-302-678-37
8	236.5	11.5	1212	7	US-11-242-505A-16
9	236.5	11.5	1212	7	US-11-242-505A-17

10	207.5	10.1	1143	7	US-11-302-678-21	Sequence 21, Appl
11	207.5	10.1	1182	7	US-11-302-678-19	Sequence 19, Appl
12	207	10.1	1152	7	US-11-304-129-35	Sequence 35, Appl
13	207	10.1	4052	7	US-11-312-958-5	Sequence 5, Appl
14	206.5	10.1	1105	7	US-11-312-958-23	Sequence 23, Appl
15	206	10.1	1727	7	US-11-312-958-11	Sequence 11, Appl
16	205.5	10.0	1179	7	US-11-304-129-39	Sequence 39, Appl
17	204	10.0	1107	7	US-11-302-678-60	Sequence 60, Appl
18	204	10.0	1670	6	US-10-511-937-449	Sequence 449, App
19	204	10.0	1670	7	US-11-302-678-58	Sequence 58, Appl
20	199.5	9.7	2139	6	US-10-511-937-338	Sequence 338, App
21	197.5	9.6	1186	6	US-10-533-300-2	Sequence 2, Appli
22	197.5	9.6	1239	7	US-11-242-505A-13	Sequence 13, Appl
23	197.5	9.6	1239	7	US-11-242-505A-14	Sequence 14, Appl
24	196.5	9.6	1143	7	US-11-304-129-51	Sequence 51, Appl
25	196.5	9.6	1179	7	US-11-304-129-2	Sequence 2, Appli
26	196.5	9.6	1179	7	US-11-304-129-3	Sequence 3, Appli
27	196.5	9.6	1182	7	US-11-312-958-7	Sequence 7, Appli
28	195.5	9.5	1170	7	US-11-302-678-34	Sequence 34, Appl
29	195.5	9.5	1170	7	US-11-302-678-36	Sequence 36, Appl
30	195	9.5	1266	7	US-11-304-129-46	Sequence 46, Appl
31	190.5	9.3	1080	7	US-11-257-851A-74	Sequence 74, Appl
32	190	9.3	1578	6	US-10-473-173-20	Sequence 20, Appl
33	189.5	9.3	1179	7	US-11-304-129-50	Sequence 50, Appl
34	182.5	8.9	1679	6	US-10-473-173-65	Sequence 65, Appl
35	182.5	8.9	1679	6	US-10-505-928-746	Sequence 746, App
36	182.5	8.9	1679	6	US-10-511-937-428	Sequence 428, App
37	182.5	8.9	1679	6	US-10-511-937-2896	Sequence 2896, Ap
38	182.5	8.9	1679	6	US-10-511-937-2918	Sequence 2918, Ap
39	175	8.5	1281	6	US-10-511-937-632	Sequence 632, App
40	173	8.4	3655	6	US-10-511-937-346	Sequence 346, App
41	172.5	8.4	50000	6	US-10-528-659-2	Sequence 2, Appli
42	165.5	8.1	2810	7	US-11-305-477-2	Sequence 2, Appli
43	164	8.0	891	7	US-11-257-851A-72	Sequence 72, Appl
44	161.5	7.9	3100	7	US-11-145-307A-183	Sequence 183, App
45	160.5	7.8	1750	7	US-11-242-111-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-11-242-505A-26  
; Publication 26, Application US/11242505A  
; Sequence No. US2006099656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; FILE REFERENCE: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, c  
; CURRENT APPLICATION NUMBER: US/11/242, 505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290, 078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347, 949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320, 351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341, 606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1173)  
US-11-242-505A-26

Alignment Scores:

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Pred. No.: 3,49e-120 Length: 1173
Score: 1366.50 Matches: 266
Percent Similarity: 78.1% Conservative: 40
Best Local Similarity: 67.9% Mismatches: 83
Query Match: 66.7% Indels: 3
DB: 7 Gaps: 2

US-10-626-445-8 (1-391) x US-11-242-505A-26 (1-1173)

QY 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
Db 1 ATCCGAGATACTAATAGCACAAATTTATCTACTAAGCACTCGTGTTAGCAATTT 60
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTACCTTTTGTCTATATCTAGGAATGCTTTGGTCATTTAGCTTTT 120
QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTTTCTTAACCTGGCCATCTCT 180
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTTTGGGTGTGATCTCAATTCCTTTGTACATCCCTCACAGCTGTTCGAATGG 240
QY 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrIleLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTGTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTATAGAACTCAACATACTGGGGTCTTGAAGATTCTTACTCTGATGGTGGTGGTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTCTGGCCCTCTTAGTGAATGGGCCAATGATCTAGTTTCAGAGCTTTCGAAGATGAA 480
QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGCCATCACA 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTGATCCCGATCATCTTAGTCGCTTATTTCACACATGAATATTAT 594
QY 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCTGTGGAAAGCGGTGCTCTCAGTAGGTGCCAAAGCCATCTCGACTGACTGCT 654
QY 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAACATCTGTGGACATCTCATTGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 241 ProGlyLeuLysGluSerAlaIleSerArgHisSerGluSerProArgArgLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCTCGCATCTCTTCAATTCAGAGAGACGGAGGAGAAAGTAGT 774
QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTTCCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834
QY 281 PheTrpArgSerGluSerAlaIleLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 835 TTTCTCCCAATCAGATTCTGATGCTCTTCCACAAAGGGAACATGTTGAATGCTTAGAGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGTTGCTGGGCTCCA 954
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QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 955 TATTCTCTGTTTCAAAATTTGCTTTTCAATTTATTTCTCTCAGCAACAGGTCCTAAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGAATTCATTTTGGCTTCAGTGTCAATTCCTTTGTCATCTCTTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCAATTGTCACAGGCTTTCAAGGCTTTCTTGAAATATTTGTATAAAAAAGCAA 1134
QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTCTACCATCAACACACAGTCGGTCAGTATCTTCT 1170

RESULT 2
US-11-242-505A-25
; Sequence 25, Application US/11242505A
; Publication No. US2006009656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310
; FILE REFERENCE: MPI2001-288P1RCP10NMIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-242-505A-25

Alignment Scores:
Pred. No.: 3,9e-120 Length: 1265
Score: 1366.50 Matches: 266
Percent Similarity: 78.1% Conservative: 40
Best Local Similarity: 67.9% Mismatches: 83
Query Match: 66.7% Indels: 3
DB: 7 Gaps: 2

US-10-626-445-8 (1-391) x US-11-242-505A-25 (1-1265)

QY 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
Db 55 ATCCGAGATACTAATAGCACAAATTTATCTACTAAGCACTCGTGTTAGCAATTT 114
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 115 TTTATGTCCTTAGTACCTTTTGTCTATAATGCTAGGAATGCTTTGTCATTTAGCTTTT 174
QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 175 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTTTCTTAACCTGGCCATCTCT 234
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 235 GACTTCTTTTGGGTGTGATCTCAATTCCTTTGTACATCCCTCACAGCTGTTTGAATGG 294
QY 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100
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Db 295 GATTTTGGAAAGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACGCA 354
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 355 TCTGTATATAACATTTGCTCTCATCAGCTATCATGATACCTGTGCTCAGTCTCAAAATGCTGTG 414
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140
Db 415 TCTTATAGAACTCAACATCTGAGTGGGGTCTTGAAGATTTGTTACTCGATGGTGGTCTTTGG 474
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 475 GTGCTGGCTCTTCTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGAAGATCAA 534
Qy 161 ThrAsnThrLysAspCysGlyProGlyPheValThrGluTyrPheIleLeuThr 180
Db 535 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATCATCTTGGCCATCACA 588
Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 589 TCATCTCTTGGAAATTCGTGATCCCATCTTCTAGTCGCTTATTTCAACATCAATATTAT 648
Qy 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 649 TGGAGCTGTGGAGCGGTGCTGCTCAGTAGGTGCCAAAGCCATCTGGACTCAGCTGCT 708
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 709 GTCTCTTCCAACTCTGTGGACACTCATTAGAGGTAGACTATCTTCAAGGAGATCTCTT 768
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 769 TCTGCATCGACAGAAAGTTCTTCGCATCTCTTCAATTCAGAGACCGAGGAGAAAGTAGT 828
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 829 CTCATGTTTCTCAGAACCAAGATGAATAGCAATACATGTTCTTCAAAATGGTGTCC 888
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 889 TTCTCCCAATCAGATTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTGTAGAGCC 948
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 949 AGGAGATTAGCAAGTCACTGGCCATTCTCTTAGGGGTTTTTGTGTTGTGGGCTCCA 1008
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 1009 TATTCTCTGTTCAAAATGTCCTTTCATTTTATTTCTCAGCAACAGGTCTTAAATCAGTT 1068
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1069 TGGTATAGAAATTCATTTGGCTTCAGTGGTTCAATTCCTTTGTCATCTCTTTTGTAT 1128
Qy 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1129 CCATTGTGTACAAAGCGTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAGCAAA 1188
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1189 CCTCTACATCAACAACAGTCGTGCTAGTATCTTCT 1224
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## RESULT 3

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US-10-511-937-2881
; Sequence 2881, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
```

```
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2881
; LENGTH: 1847
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2881
Alignment Scores:
Pred. No.: 5,68e-19 Length: 1847
Score: 297.50 Matches: 100
Percent Similarity: 43.5% Conservative: 62
Best Local Similarity: 26.9% Mismatches: 120
Query Match: 14.5% Indels: 91
DB: 6 Gaps: 14
US-10-626-445-8 (1-391) x US-10-511-937-2881 (1-1847)
Qy 13 AlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGly 32
Db 571 GCATGCAAGATCACCATCCGTCGTCTTGGCGTCTCATCTCCATCATCACCGTTGCTGCG 630
Qy 33 AsnAlaValValIleLeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyr 52
Db 631 AATGTGTGTCTGTCTGTGGCGGTGTGAACCGCGGCTTCCGCAACCTGACCAATGTGT 690
Qy 53 PhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeu--- 71
Db 691 TTCATCGTGTCTGTGGCTATCAGTACCTGTCTCTCGGCTCTGCTGCTGCTCTCTCT 750
Qy 72 TyrIleProHisValLeuPheAsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeu 91
Db 751 GCCATCTACCAAGTCTCTCAAGTGGAGCTTTGGCAAGGTCTTCTGCAATATCTACACC 810
Qy 92 IleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAsp 111
Db 811 AGCTGTGATGTGATGCTCTGCACAGCTCCATCTTAACTCTTTCATGATCAGCTTCGAC 870
Qy 112 ArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLys 131
Db 871 CGGTACTGCGCTGTCAAGCCACTCGGTACCTGTGTGGTCAACCCAGTT---CGG 927
Qy 132 IleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIle 151
Db 928 GTGCCATCTCTCTGTGTTAAATTTGGTTCATCTCCATTACCTGCTCTTCTGTCTATC 987
Qy 152 LeuAlaSerAspSerTrpLysAsnSerThrAsn-----ThrLysAspCys 166
Db 988 CACCTGGGTGGAAACAGCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1047
Qy 167 GluProGlyPheValThrGluTyrTrpIleLeuThrIleThrMetLeuLeuGluPheLeu 186
Db 1048 AAGTCCAG---GTCAATGAAGTACAGGGCTG---GTGGATGGGCTGGTCACTCTCTAC 1101
Qy 187 LeuProValIle-SerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysAr 206
Db 1102 CTCCTGCTACTGATCA----- 1117
Qy 206 gArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerAlaSe 226
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Qy 255 ProhArgLysSerSerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThr 274
Db 772 AAGCACAGCAGGAAGGCGCTGAAGCGCAGCGCTG----- 804
Qy 275 AlaPheLysValGlySerPheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyr 294
Db 804 ----- 804
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 805 -----ACGCTGGGCATCTGCTGGGCATGTC 831
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 832 TTTGTGACCTGGTGGCTCTTTGTGGCCAAACATAGTCACAGGCGTG-----TGC 882
Qy 335 GluArgProLysSerValTyrTrpSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 883 GACTGCATCTCCCGAGCGCTTCGATGTCTCATATGGCTGGGTACTGTAAACAGCACC 942
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 943 ATGAACCCCATCTACTCCCACTCTTCATGCGGACTTCAAGCGGCGCTGGGCAGGTTC 1002
Qy 375 LeuCysValThrLysTrpPro 381
Db 1003 CTGCCATGTCCAGCGCTGCC 1023

RESULT 5
US-11-302-678-40
; Sequence 40, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (468) ... (1790)
; US-11-302-678-40
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Alignment Scores:
Pred. No.: 8,75e-19 Length: 1984
Score: 296.00 Matches: 103
Percent Similarity: 41.1% Conservative: 65
Best Local Similarity: 25.2% Mismatches: 136
Query Match: 14.5% Indels: 105
DB: 7 Gaps: 12

US-10-626-445-8 (1-391) x US-11-302-678-40 (1-1984)

Qy 4 SerAsnSerThr-----GlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
Db 492 GCCAATAGCACCCCGCGCTGGGGGAGGGCGCGCGCTGGCGCCCGGGGGGAGCGGCTGG 551
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetVal-----GlyAsnAlaValIle 37
Db 552 GTGGCGCCCGCGCTGTGGTGGTGCATCGCTGAGCGCGCGCGCAACTCGCTGCTGATC 611
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 612 GCGCTCATCTGCACCTCAGCCCGCGCTGCGCAACACAGTCCAACCTTCTTCTGCTGCTC 671
Qy 58 AlaIleSerAspPheLeuValGlyIleSerIleProLeuTyrIleProHisValLeu 77
Db 672 TTCACGCTCAGCTGATGGTGGGCTGGTGTATGCCGCGCCATGCTGTAACGCGCTG 731
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 732 TAGGGCGCTGGGTGGTGGCGCGCGCTGTGCTGTCTGGACCGCTTCGAGTGTATG 791
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 792 TGTGTCAGCGCTCCATCTCAACCTCTGCTCATCAGCTGGACCGCTACCTGCTCATC 851
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMet 136
Db 852 CTCTCGCGCTGGCTGACAGCTGCGCATCAGCGCC---CTGCGTGGCGCTGGCGCTAGTC 908
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGly---ProMetIleLeu-AlaSerAs 155
Db 909 CTGGCGCGCTGGAGCGCTCGCGCTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTG 968
Qy 155 pSerTrpLysAsn-----SerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 969 GAGCTGGCGCACGACGCGCCAGTCCCTGGCGAGTCCGCTGCTGCTGCTGCTGCTGCT 1028
Qy 171 lThrGluTrpTyrIleLeuThrIleThrMetLeuLeuLeuLeuProValIleSe 191
Db 1029 TTTG----- 1032
Qy 191 rValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAlaLeuSerAr 211
Db 1033 -----TCTTGTGGCGTGGCGCTCACCTTCTTC 1061
Qy 211 gCysProSerHisAlaGlyPheSerThrThrSerSerSer-AlaSer----- 226
Db 1062 CTGCTCTGGGTGCGCATATGCTTTCACCTACTGACAGGATCTGCTAGTGTGCGCGCAG 1121
Qy 227 -----GlyHisLeuHisArg-AlaGlyValAlaCys----- 236
Db 1122 GCGCTGAGTGGCTGCTCCCTCACCCCGGATGGCCAGTGGCGCTCGGAGACGCTGAG 1181
Qy 237 -----ArgThrSerAsnProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSer 254
Db 1182 GTGCCAGGACCCCGCCCGCGGGGTG---GAGTCTGCTACAGCAGCGCTGCTAGCAGC 1238
Qy 255 ProArgArgLysSerSerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThr 274
Db 1239 AAGCACAGCAGGAAGGCGCTGAAGCGCGCTG----- 1271
Qy 275 AlaPheLysValGlySerPheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyr 294
```

```
Db 1271 ----- 1271
QY 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1272 -----ACGCTGGGCATCTCTGGGCATGTTTC 1298
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1299 TTTGTGACCTGGTGGCTTCTTTGTGGCCAAACATAGTCCAGGCCGTG-----TGC 1349
QY 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1350 GACTGCATCTCCCGAGCCCTCTTCGATGCTCTCACATGGCTGGGTACTGTAAACAGCACC 1409
QY 355 ValAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1410 ATGAACCCCATCATCACCACTCTTCATCGGGGACTTCAAGCGGGCGCTGGGCAGGTTTC 1469
QY 375 LeuCysValThrLysTrpPro 381
Db 1470 CTGCCATGTCCAGCTGTCCC 1490

RESULT 6
; Sequence 39, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1074)
US-11-302-678-39

Alignment Scores:
Pred. No.: 3,93e-19 Length: 1074
Score: 295.50 Matches: 88
Percent Similarity: 44.1% Conservative: 72
Best Local Similarity: 24.2% Mismatches: 134
```

```
Query Match: 14.4% Indels: 69
DB: 7 Gaps: 14
US-10-626-445-8 (1-391) x US-11-302-678-39 (1-1074)
QY 18 LeuAlaPheLeuMet---SerSerPheAlaPheAlaIleMetValGlyAsnAlaValVal 36
Db 139 CTGGGCTTTCTGTGGCGGCGAGTTCGCGTGAACCTGCTGGTG----- 183
QY 37 IleLeuAlaPheValValAspArgAsnLeuArgHisArg---SerAsnTyrPhePheLeu 55
Db 184 ---CTGGCGACCATCTCTCGGTGTACGACCTTCCACCGCGTGCACACCTGGTGGCA 240
QY 56 AsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHis 75
Db 241 TCCATGGCGCTCTCGATGTCTGTGGTGGCGCGCTGTCATGCGCTGAGCCCTGGTGCAT 300
QY 76 ValLeuPhe-----AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThr 93
Db 301 GAGCTGTCCGGGCGCGCTGGCAGTAGGTTCGAGGCTGTGCCAGCTTTGGATCGCGTGC 360
QY 94 AspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyr 113
Db 361 GAGTGTCTTGTGTGCACGCCGACATCTGGAACGTGACGGCCATAGCCCTGGACCGGTAC 420
QY 114 GlnSerValSerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleVal 133
Db 421 TGGTCCATCAGCGCGCACATGGAATACACGCTCCGACCGCGAAGTGCCTCCACAGTC 480
QY 134 AlaGlnMetValAlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeu 152
Db 481 -----ATGATCGCGCTCACCTGGGCACCTTCCGCTGTCTCTCTGGCCCCGCGCTT 534
QY 153 AlaSerAspSerTrpLysAsnSerThrAsnThrLysAspCys-----GluPro 168
Db 535 TTTGGCTGGGGAGAGACGTACTCTGAGGGCAGCGAGAGTCCAGGTAAAGCCCGAGCCT 594
QY 169 GlyPheValThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuPro 188
Db 595 TCCTACGCC-----GTGTTCTCCACCGTAGGCGCCTTCTACCTGCCG 636
QY 189 ValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAla 208
Db 637 CTCTGTGTGTGTCTCTTC-----GTGTACTGGAAGATCTACAAGGTGCC--- 681
QY 209 LeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerAlaSerGlyHis 228
Db 681 ----- 681
QY 229 LeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuLysGluSerAlaA 248
Db 682 -----AAGTTCGCGTGGGCTCCAGGAAGACCAATAGCGTCTCACCCATATCGAAGCT 735
QY 249 SerArgHisSerGluSerProArgArgLysSerSerIleLeuValSerLeuArgThrHis 268
Db 736 GTGGAGGTGAAGGACTCTGCCAAACACGCCAGTGTGTTC-----ACGGTC 783
QY 269 MetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArgSerGluSerAlaA 288
Db 784 CGCCAGCCACCTCCACTTCCAGCCAGAGGGGACACGTGGCGGGAGCAG----- 834
QY 289 LeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAla 308
Db 835 -----AAGAGCAGCGCGCGCGCCTCATGGTGGCG 864
QY 309 IleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeu 328
Db 865 ATCCTCATTTGGCGTGTGTGTCTCTGCTGATCCCCCTTTCTTC---ACCGAGCTCATC 921
QY 329 SerThrTyrProArgThrGluArgProLysSerValTrpTyrSerIleAlaPheTrpLeu 348
Db 922 AGTCCCTCTGCTCTGTGTGACATCCCC---GCCATCTGGAAGCATCTTCTCTGCTGCTT 978
```



```

Qy 349 GlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisArgArgPheGln 368
Db 979 GGCTACTCCCAACTCCTCTTTAAACCCCTGAICTATACGGCTTTCAACAAGAACTACAAC 1038
Qy 369 LysAlaPhe 371
Db 1039 AGCGCCTTC 1047

RESULT 7
US-11-302-678-37
; Sequence 37, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1137)
US-11-302-678-37

Alignment Scores:
Pred. No.: 4,4e-19 Length: 1159
Score: 295.50 Matches: 88
Percent Similarity: 44.1% Conservative: 72
Best Local Similarity: 24.2% Mismatches: 134
Query Match: 14.4% Indels: 69
DB: 7 Gaps: 14

US-10-626-445-8 (1-391) x US-11-302-678-37 (1-1159)

Qy 18 LeuAlaPheLeuMet---SerSerPheAlaPheAlaIleMetValGlyAsnAlaValVal 36
Db 202 CTGGCGCTTCTGGTGGCGGACGCTTCCTGGAACTCTGCTGGTG----- 246
Qy 37 IleLeuAlaPheValAspArgAsnLeuArgHisArg---SerAsnTyrPhePheLeu 55
Db 247 ---CTGGCGACCATCTCTCCGTGTACGACCTTCACCGCGTGGCCCAACACCTGGTGCA 303
Qy 56 AsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHis 75

```

## RESULT 8

```

US-11-242-505A-16
; Sequence 16, Application US/11242505A
; Publication No. US2006009665A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.

```

```

Db 304 TCCATGCGCGTCTCGGATGTCCTGGTGGCGCGGTGGTGCATGCGCGTGAGCGCTGGTGCAT 363
Qy 76 ValLeuPhe-----AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThr 93
Db 364 GAGCTGTCGGGGCGCGCTGGCAGCTAGTTCGGAGGCTGTGCCAGCTTTGGATCGCGTCG 423
Qy 94 AspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyr 113
Db 424 GACGTGCTTTGCTGCACGGCCAGCATCTGGAACCTGACGGCCATAGCCCTCGACCGCTAC 483
Qy 114 GlnSerValSerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleVal 133
Db 484 TGTTCATACGGCCACATGGAATACCGTCCGCACCCCAAGTGGGTCTCCACAGTC 543
Qy 134 AlaGlnMetValAlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeu 152
Db 544 -----ATGATCGCGCTCACCTGGGCATCTCCGCTGTGCATCTCTTGGCCCGCTGCTT 597
Qy 153 AlaSerAspSerTrpLysAsnSerThrAsnThrLysAspCys-----GluPro 168
Db 598 TTTGGCTGGGGAGAGACGTACTCTGAGGGCAGCAGGAGGTGCCAGTAAGCCGAGCGCT 657
Qy 169 GlyPheValThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuPro 188
Db 658 TCCTACGCC-----GTGTTCTCCACCGTAGGCGCTTCTACTGCGCG 699
Qy 189 ValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAla 208
Db 700 CTCGTGTGTGTCTTTC-----GTGTACTGGAAGATCTACAAGCTGCC--- 744
Qy 209 LeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerSerAlaSerGlyHis 228
Db 744 ----- 744
Qy 229 LeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuLysGluSerAlaAla 248
Db 745 -----AAGTTCGCGTGGGCTCCAGGAAGCAACATAGCGTCTCACCCTATTCGAAGCT 798
Qy 249 SerArgHisSerGluSerProArgArgLysSerSerIleLeuValSerLeuArgThrHis 268
Db 799 GTGGAGGTGAAGGACCTTCGCCAAACACGCCCCAGATGGTGTTTC-----ACGGTC 846
Qy 269 MetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArgSerGluSerAlaAla 288
Db 847 CGCACGCCACCGTCACCTTCCAGCCAGAAAGGGACACGTCGGCGGAGCAG----- 897
Qy 289 LeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAla 308
Db 898 -----AAGGAGCAGCGCGCGCCCTCATGCTGGGC 927
Qy 309 IleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeu 328
Db 928 ATCTCATTCGGGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
Qy 329 SerThrTyrProArgThrGluArgProLysSerValTrpTyrSerIleAlaPheTrpLeu 348
Db 985 AGTCCCTCTGCTCCTGTGACATCCCC---GCCATCTGGAAGAAAGCATCTTCTCTGGGCTT 1041
Qy 349 GlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisArgArgPheGln 368
Db 1042 GGCTACTCCCAACTCCTCTTTTAAACCCCTGATCTATACGGCTTTCAACAAGAACTACAAC 1101
Qy 369 LysAlaPhe 371
Db 1102 AGCGCCTTC 1110

```





[illegible]

```
QY 50 SerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIle 69
Db 293 ACCAACATTTACATATTAACTGGCTTGGCAGATGCTTAGTT--ACTACAAACCATG 349
QY 70 ProLeuTyrIleProHisValLeuPheAsn--TrrAsnPheGlySerGlyIleCysMet 88
Db 350 CCCTTTTCAGAGTACGGTCTACTTGATGATTCCTGGCTTTGGGGATGGCTGTGCAAG 409
QY 89 PheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIle 108
Db 410 ATAGTAATTTCCATTTGATTTACTCAACATGTTCCACGACATCTTCACCTTGACCATGATG 469
QY 109 SerTyrAspArgTyrGlnSerValSerAsn-----AlaValSerTyrArgAlaGln 125
Db 470 AGCGTGACCGCTACATTTGGCGTGTGCACCCCGCTGAAGGCTTTGGACTTCCGCACACCC 529
QY 126 HisThrGlyIleMetIleValAlaGlnMetValAlaValTrrIleLeuAlaPheLeu 145
Db 530 -----TTGAAGGCAGAAATCATCAATATCTGCATCTGGCTGTGCTGCATCT 577
QY 146 ValAsn---GlyProMetIleLeuAlaSerAspSerTrpIysAsnSerThrAsnThrLys 164
Db 578 GTTGGCATCTCTGCATATAGTCTTGGAGGCACCAAGTCAGGAGACGTCGATGTCAAT 637
QY 165 AspCysGluProGlyPheValThrGluTrrTyrIleLeuThrIleThrMetLeuLeuGlu 184
Db 638 GAGTGTCTCTGAGTTCCTCCAGATGATGACTAC----- 670
QY 185 PheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrp 204
Db 671 -----TCTGTGGGACCTCTTC 688
QY 205 Lys-ArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerSe 224
Db 689 ATGAAGATCTGCGTCTTCATCTTTGCCTTCGTGATCC----- 725
QY 224 rAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuLy 244
Db 726 -----CTGTC 730
QY 244 sGluSerAlaAlaSerArg-HisSerGluSerPro-ArgArgIysSerSerIleLeuVal 263
Db 731 CTATCATCATCTGCTGCTACCTGATGATCTCGTCTCAAGACGTCGCGCTCCTT 790
QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 791 TCT-----GGCTCC----- 799
QY 284 SerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeu 303
Db 800 -----CGAGAGAAAGATCGCAACCTG-----CGTAGGATC 829
QY 304 AlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeu 323
Db 830 ACCAGACTGCTGCTGGTGGTGGCGGTTTCTGCTGCTGCTGAGATCCCATTCACATA 889
QY 324 PheThrIleValLeu-----SerThrTyrProArgThrGluArgProLysSerVal 340
Db 890 TTCACTCTGTGGAGGCTCTGGGAGGACCTCCACAGACAGATGCTCTCTCCAGCTAT 949
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnPropheLeuTyr 360
Db 950 TACTTCTGCATCGCC-----TTAGGTATACCAACAGTAGTACGCTGATCCCATCTCTAC 1003
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPhe 371
Db 1004 GCCTTTCTTGATGAAAACCTTCAAGCGGTGTTTC 1036
```

RESULT 12

US-11-304-129-35

; Sequence 35, Application US/11304129

; Publication No. US2006008915A1

## GENERAL INFORMATION:

```
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; PRIOR FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 35
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Human
; US-11-304-129-35

Alignment Scores:
Pred. No.: 9,87e-11 Length: 1152
Score: 207.00 Matches: 104
Percent Similarity: 39.7% Conservative: 53
Best Local Similarity: 26.3% Mismatches: 141
Query Match: 10.1% Indels: 99
DB: Gaps: 16

US-10-626-445-8 (1-391) x US-11-304-129-35 (1-1152)
```

```
QY 13 AlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGly 32
Db 151 GCAGCCAAAGATCGTCATTTGGCATTTGCACATGCGCAGGCATCATGCTGGTCTCGCGCATCGGT 210
QY 33 AsnAlaValValIleLeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyr 52
Db 211 AACTTTGTCTTTATCGCTGCCCTCACCCGCTATAGAAGTTGCGCAACCTCACCACATCTG 270
QY 53 PhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyr 72
Db 271 CTCATTGCCAACCTGGCCATCTCGGACTTCTTGGTGGCCATCATCTGCTGCCCTTCGAG 330
QY 73 IleProHisValLeu-----PheAsnTrpAsnPheGlySerGlyIleCysMetPhe 89
Db 331 ATGGACTACTACTGTTAGTGTACGGCAGCTCTCTCTGGGAGCATGGCCACGTGCTCTGT----- 384
QY 90 TrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyr-----AsnIle 105
Db 385 ---GCCTCCCGTCACTACCTACCTGGCG---ACCGTCTCCCTCTACGCTCCACCAATGCCCTTG 438
QY 106 ValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGln 125
Db 439 CTGGCCATTGCCATTGACAGATATCTCGCATCTGTTCACTCCCTTCAAAACCAACCGATGAAT 498
QY 126 HisThrGlyIleMetIysIleValAlaGlnMetValAlaValTrrIleLeuAlaPheLeu 145
Db 499 TATCAAAACGGCCCTCTTCTCTGATCGCC-----TTGGTCTGGATGGTGTTCATCTCTC 549
QY 146 ValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrLysAsp 165
Db 550 ATTGCG-CATCCCATCGGCTTACTTTGCG-----AACAGAAACCGCTCTCTTTAT 596
QY 166 Cys---GluProGlyPheValThrGluTrrTyrIleLeuThrIle-----ThrMetLeu 182
Db 597 TGTCAAGAGCCAGGAGAGATCTTCTGTGGCCAGATCTTGTGGCTGTGGATCAGCAGCTCTA 656
```

```
183 LeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSer 202
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
657 CTCAAGTCTACTTCTCTTCA-TCITTG-----GTGTGAGTTCTGTGGCC 703
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
203 LeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrTrpSer 222
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
704 CTGTGG-----TCACCATGACC-----721
|||...|||...|||...|||...|||...|||...|||...|||...|||...
223 SerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGly 242
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
722 -----TGTGCTATGCCAGGA 736
|||...|||...|||...|||...|||...|||...|||...|||...|||...
243 LeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeu 262
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
737 TCTCCCGGAGCTCTGTTCAAGCACTCTCTGGGTTCCAGACGACC-----784
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
263 ValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrp 282
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
784 -----784
|||...|||...|||...|||...|||...|||...|||...|||...|||...
283 Arg-SerGluSerAlaAlaLeu-ArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgL 302
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
785 AGATTCCAAAGCGCTCGCTGCCG-----AGGA 814
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
302 yslLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTrpAlaProTyrC 322
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
815 AGAGGTCCTGTGCTCATGTGCATTCTACGGCTATGTGCTGTGTGGCACCTTCT 874
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
322 yslLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerValTrpT 342
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
875 ACGGTTTACCATCGTTTCGTGACTTCTTCCC---ACTGTGTTCTGTGAAGAAAGCACT 931
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
342 YrSerIleAlaPheTrp-----LeuGlnTrpPheAsnSerPheValAsnProp 358
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
932 ACCTCACTGCTTCTACGTTGGTGGTGCATCGGCATCGACACAGCATGATCAACACCG 991
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
358 heLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValT 378
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
992 TGTGCTTCTGTGACGGTCAAGAACCAACCATGAAGTACTTCAAGAAGATGATGCTGTGC 1051
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
378 hrlYsTrpProAlaLeuSerGlnAsnGlnSerValSerSer 391
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
1052 ACTGGCTGCC-----TCCAGCGGGGAGCAAGTCCAGT 1086
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
RESULT 13
US-11-312-958-5
; Sequence 5, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22445, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MPI02-027P1RNONMIN
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/11/312, 958
; PRIOR FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369, 022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360, 495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370, 121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373, 010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373, 908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377, 717
; PRIOR FILING DATE: 2002-05-03
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; PRIOR APPLICATION NUMBER: US 60/379, 949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382, 409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385, 280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386, 879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4052
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(1199)
US-11-312-958-5

Alignment Scores:
Pred. No.: 6,36e-10 Length: 4052
Score: 207.00 Matches: 104
Percent Similarity: 39.7% Conservative: 53
Best Local Similarity: 26.3% Mismatches: 141
Query Match: 10.1% Indels: 99
DB: 7 Gaps: 16

US-10-626-445-8 (1-391) x US-11-312-958-5 (1-4052)
QY 13 AlaAlaGlnValProLeuAlaPheLeuMetSerPheAlaPheAlaIleMetValGly 32
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 195 GCAGCCAGATGTCATGTGGCATGTGCACGTGGCAGGCATCATGTGGTCTGGCGCATCGT 254
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 33 AsnAlaValValIleLeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyr 52
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 255 AACTTTGTCTTTATCGTGCCTCACCGCTATAAAGAGTTGCGCAACCTCACCAATCTG 314
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 53 PhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyr 72
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 315 CTCATTGCCAACCTGGCCATCTCCGACTTCTGTGGTGGCCATCATGTGTCGCCCTTCGAG 374
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 73 IleProHisValLeu-----PheAsnTrpAsnPheGlySerGlyIleCysMetPhe 89
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 375 ATGAGTACTACTGTGTACGGCAGCTCTCTCTGGGAGCATGGCCAGCTGCTGT-----428
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 90 TrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyr-----AsnIle 105
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 429 ---GCCTCCGTCAACTACCTTCGCGC---ACCGTCTCCCTCTACGTCCTCCACCAATGCCCTTG 482
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 106 ValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGln 125
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 483 CTGGCCATTGCCATTGACAGATATCTCGCATCTGTCACCTTGAACACCGATGATGAT 542
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 126 HisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeu 145
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 543 TATCAAAAGCCCTCTTCTGATCGCC-----TTGGTCTCGATGTTGCTCCATTCTC 593
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 146 ValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrLysAsp 165
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 594 ATTGC-CATCCCATCGGCTTACTTTGC-----AACAGAAACCGTCTCTTTAT 640
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 166 Cys---GluProGlyPheValThrGluTrpTyrIleLeuThrIle-----ThrMetLeu 182
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 641 TGTCAAGAGCCAGGAGAGATCTTCTGTGGCCAGATCTGGCCTGTGGATCAGCAGCTCTA 700
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 183 LeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSer 202
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 701 CTACAAGTCTACTTCTCTTCA-TCITTG-----GTGTGAGTTCTGTGGCC 747
|||...|||...|||...|||...|||...|||...|||...|||...|||...
QY 203 LeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrTrpSer 222
|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 748 CTGTGG-----TCACCATGACC-----765
|||...|||...|||...|||...|||...|||...|||...|||...|||...
```







```
Db      ::: ||| :::::::::: |||:::||||| |||
871 ATCAAGATTGATGCTGGTAGTCTCTTTGCCCTCTGCTGGTCCCTCAACTGC 930
Qy      PheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerValTyrTyrSer 343
Db      :: ::::::::::|||::: :: ||| ::
931 TACGTCTCTCTCTCTCTCCAGC-----AAGGTCAATCCGCACCAACAATGCCCTCTACTTT 984
Qy      IleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyrProLeuCys 363
Db      ::||| :::::: |||:::|||||::: |||
985 GCCTTCCACTGGTTGGCCATGAGCAGCACCTGCTATACCCCTTCATATACTGCTGGCTG 1044
Qy      HisArgArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyrProAlaLeu 383
Db      :: |||::: ::||| :::: ||| ::: |||
1045 AACGAGAACTTCAGGATTGAGCTAAAGGCATTACTGACGATGTGTCAAGACCTCCCAAG 1104
Qy      SerGlnAsnGlnSerValSerSer 391
Db      |||
1105 CCTCAGGAGGACGGCAACCCCTCC 1128
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Search completed: May 25, 2006, 15:34:49  
Job time : 70 secs

